

- AI141736
F-NT2RM2000556//ESTs//3.1e-33:183.96//Hs.136990:AA769220
F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751.97//Hs.74369:AF032108
5 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508
F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128
F-NT2RM2000577//ESTs. Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214.92//Hs.55609:W37993
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987
10 F-NT2RM2000588//ESTs//1.5e-33:183.97//Hs.136990:AA769220
F-NT2RM2000594
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313
15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217-AA846548
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272
20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576
F-NT2RM2000669//ESTs//1.3e-56:283.98//Hs.156342:AI337371
25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748.64//Hs.7938:D86984
F-NT2RM2000718//Homo sapiens mRNA for HRHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342
30 F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756.82//Hs.74107:X59244
F-NT2RM2000740//ESTs. Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286
F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750
F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338
F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701
35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046
F-NT2RM2000952//ESTs. Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:AI023761
F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433
40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831
F-NT2RM2001035//ESTs. Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.17035:AI080471
F-NT2RM2001065
F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258
45 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190
F-NT2RM2001141
50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042
F-NT2RM2001177
F-NT2RM2001194//ESTs. Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630
55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

AF039694
F-NT2RM2001256
F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845
F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601
5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615
F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605
F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567
F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706
10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905
F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322
F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382
F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:
15 AJ007509
F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303
F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903
F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969
F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459
20 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262
F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800
F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902
25 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729
F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431
F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918
30 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518
F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952
F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725
35 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301
F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195
40 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907
F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129
45 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356
F-NT2RM2001675
F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305
F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216
50 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937
F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826
55 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA107788
F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
F-NT2RM2001718
F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931

F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132

5 F-NT2RM2001743

F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399

F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

10 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742

F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933

F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698

F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens IkkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

20 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H. sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:96//Hs.113283:AF018080

25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610

30 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLC1101133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931

35 F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840

F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080

40 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392

F-NT2RM2001982

F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816

F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778

45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538

F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398

F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274

F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729

50 F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516

F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427

F-NT2RM2002055//ESTs//1.1e-91:453:99//Hs.158370:AI382154

F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377

F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840

55 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435

F-NT2RM2002128

- F-NT2RM2002142//ESTs//0.0031:183.66//Hs.144505:AA575724
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144.800:92//Hs.20815:AF084928
 5 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787.97//Hs.11147:AB007936
 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291.61//Hs.99936:X14487
 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610.59//Hs.148027:X63563
 10 F-NT2RM4000027//ESTs//1.6e-64:352.94//Hs.21331:H93074
 F-NT2RM4000030//ESTs//1.0:115.63//Hs.131055:AI391464
 F-NT2RM4000046//ESTs//2.6e-09:207.65//Hs.14353:AI094674
 F-NT2RM4000061//ESTs//0.89:207.60//Hs.98445:AI038511
 F-NT2RM4000085//ESTs. Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H. sapiens]//1.6e-30:369.70//Hs.114623:AI204280
 15 F-NT2RM4000086
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345.69//Hs.13128:AF060865
 F-NT2RM4000139
 F-NT2RM4000155
 20 F-NT2RM4000156//ESTs//5.9e-73:345.100//Hs.155958:AA573632
 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676.61//Hs.159228:AF041853
 F-NT2RM4000169//ESTs//2.0e-103:483.99//Hs.43729:AA497044
 F-NT2RM4000191//TRICHOHYALIN//0.011:324.60//Hs.82276:L09190
 25 F-NT2RM4000197//ESTs//1.5e-48:311.88//Hs.136144:W27744
 F-NT2RM4000199//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
 F-NT2RM4000200
 F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424.60//Hs.91400:AB006626
 30 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856.98//Hs.111138:AB018255
 F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358.60//Hs.75055:M93651
 F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572.60//Hs.47061:AF045458
 35 F-NT2RM4000233//ESTs//2.0e-37:269.85//Hs.148873:T33582
 F-NT2RM4000244//EST//0.83:319.57//Hs.162412:AA573439
 F-NT2RM4000251//ESTs. Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112.92//Hs.93841:AA442297
 40 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229.83//Hs.46328:D87942
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609.93//Hs.31305:M99438
 F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460.59//Hs.5372:AB000712
 45 F-NT2RM4000327//ESTs//0.019:269.60//Hs.153697:AI240707
 F-NT2RM4000344//ESTs. Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432.95//Hs.12796:W27884
 F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666.68//Hs.155291:D13630
 50 F-NT2RM4000354//ESTs. Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55.92//Hs.59075:M023761
 F-NT2RM4000356//ESTs//1.0:225.60//Hs.161175:AI418425
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628.99//Hs.8152:AB014542
 F-NT2RM4000368//ESTs//4.9e-13:323.63//Hs.143695:AA662745
 55 F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843.68//Hs.23796:AL022718
 F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166.65//Hs.946:X73029

- F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114.94//Hs.137580:AB015046
- F-NT2RM4000421
- 5 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432.74//Hs.154872:AB011166
- F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543.58//Hs.2175:M59820
- F-NT2RM4000457
- F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:176.631//Hs.66369:U95040
- 10 F-NT2RM4000486//ESTs//9.2e-48:237.99//Hs.160685:AI280004
- F-NT2RM4000496//ESTs//0.069:252.61//Hs.155958:AA573632
- F-NT2RM4000511//EST//0.92:191.58//Hs.61517:AA028915
- F-NT2RM4000514
- F-NT2RM4000515//ESTs//7.3e-93:450.98//Hs.120975:AA034409
- 15 F-NT2RM4000520//ESTs//0.13:183.65//Hs.144828:AI221305
- F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756.96//Hs.125870:AI364967
- F-NT2RM4000532//ESTs//7.7e-43:388.78//Hs.105665:H78987
- F-NT2RM4000534
- 20 F-NT2RM4000558
- F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593.62//Hs.7764:AB007938
- F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532.96//Hs.6092:T75227
- 25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305.68//Hs.40100:AB002390
- F-NT2RM4000611//EST//0.76:268.58//Hs.150031:AI292068
- F-NT2RM4000616
- F-NT2RM4000674
- F-NT2RM4000689
- 30 F-NT2RM4000698//Apolipoprotein E//1.0:290.59//Hs.76260:M12529
- F-NT2RM4000700
- F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744.77//Hs.42400:AF022789
- F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771.97//Hs.6823:W18181
- 35 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257.60//Hs.957:M84605
- F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743.98//Hs.137168:AB018303
- F-NT2RM4000741
- 40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388.96//Hs.112361:R99396
- F-NT2RM4000764//ESTs//3.8e-104:539.95//Hs.24739:H67815
- F-NT2RM4000778//ESTs//1.5e-85:419.97//Hs.99838:AA204731
- F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810.98//Hs.18586:AB007920
- 45 F-NT2RM4000787//EST//0.011:182.65//Hs.159928:AA969186
- F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736.98//Hs.25817:AC005306
- F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160.80//Hs.124902:AI337820
- 50 F-NT2RM4000796//Human K⁺ channel subunit gene, complete cds//0.96:292.62//Hs.124212:M64676
- F-NT2RM4000798//ESTs//1.9e-34:271.82//Hs.128203:AA972301
- F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kd subunit (SNAP190) mRNA, complete cds//0.052:238.64//Hs.113265:AF032387
- F-NT2RM4000820//ESTs//0.053:274.61//Hs.23748:H16568
- 55 F-NT2RM4000833
- F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374.61//Hs.7841:AB002322
- F-NT2RM4000852//EST//1.0:222.60//Hs.120354:AA718934
- F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

- ensj/4.4e-29:164.95//Hs.115095:AI392943
F-NT2RM4000887
- 5 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407.64//Hs.21293:AB011004
F-NT2RM4000950
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571.77//Hs.7289:AB007875
F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381.67//Hs.2481:X78926
- 10 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803.98//Hs.19542:AB018272
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584.99//Hs.15711:AB014539
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469.58//Hs.5333:AB018254
- 15 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340.92//Hs.87310:AI247543
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//0.79:142.69//Hs.77424:M63835
F-NT2RM4001084
- 20 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235.62//Hs.108947:D30758
F-NT2RM4001116
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225.61//Hs.134989:L12701
F-NT2RM4001151//ESTs//1.1e-07:190.65//Hs.151691:AA443730
F-NT2RM4001155//ESTs//2.2e-12:181.74//Hs.128826:AI004145
- 25 F-NT2RM4001160//EST//0.83:166.61//Hs.117051:AA677351
F-NT2RM4001187
F-NT2RM4001191//ESTs//1.3e-42:248.93//Hs.13475:R18220
F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799.69//Hs.2479:X78933
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707.99//Hs.14934:AF004828
- 30 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291.62//Hs.31582:AA877205
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715.70//Hs.104925:AF059611
- 35 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208.96//Hs.26676:AA033997
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435.59//Hs.6360:AB007950
F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356.59//Hs.26971:AC003003
- 40 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474.89//Hs.32971:Z46973
F-NT2RM4001316//ESTs//1.2e-14:126.84//Hs.154344:AA258335
F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642.66//Hs.87435:D89016
F-NT2RM4001340//EST//0.40:135.70//Hs.161198:AA18988
- 45 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284.58//Hs.120997:R56714
F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818
F-NT2RM4001371//EST//0.52:262.59//Hs.145991:AI277656
- 50 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790.98//Hs.5151:AF098799
F-NT2RM4001384
F-NT2RM4001410//ESTs//1.1e-47:290.91//Hs.72447:AA160575
F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475.64//Hs.105052:AB000520
F-NT2RM4001412
- 55 F-NT2RM4001414//ESTs, Moderately similar to 18547_1 [H.sapiens]//5.2e-18:133.87//Hs.28209:AI073817
F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611.70//Hs.154326:D42087
F-NT2RM4001444
F-NT2RM4001454//ESTs//3.9e-31:169.96//Hs.117982:AA644658

- F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784
 5 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247
 F-NT2RM4001557
 10 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859
 F-NT2RM4001582
 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094
 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077
 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334
 20 F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739
 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946
 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339
 25 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957
 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306
 F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719
 35 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270
 40 F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712
 45 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687
 F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204
 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814
 F-NT2RM4001856
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711
 55 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984
 F-NT2RM4001880
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

- F-NT2RM4001922//ESTs//2.5e-51:291.93//Hs.26660:AI312633
 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359.57//Hs.155356:AJ224875
 F-NT2RM4001938
 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808.98//Hs.118631:AF098162
 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362.83//Hs.154326:D42087
 F-NT2RM4001965//ESTs. Weakly similar to KIAA0157 gene product is novel. [H.sapiens]/1.8e-65:337.96//Hs.130135:AA905493
 10 F-NT2RM4001969//ESTs//0.00024:261.63//Hs.157579:AI312862
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527.76//Hs.159277:AB018341
 F-NT2RM4001984//EST//7.1e-05:235.61//Hs.105444:AA508082
 F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181.65//Hs.11147:AB007936
 15 F-NT2RM4002013//ESTs//0.97:185.63//Hs.103345:AI302271
 F-NT2RM4002018//ESTs//2.5e-76:398.94//Hs.119544:T95601
 F-NT2RM4002034
 F-NT2RM4002044//ESTs//9.6e-83:410.97//Hs.128162:AA815048
 F-NT2RM4002054//EST//8.5e-12:176.71//Hs.137181:R56912
 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803.98//Hs.153026:AB014540
 F-NT2RM4002062//ESTs. Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //7.0e-94:396.94//Hs.59346:AI126802
 F-NT2RM4002063
 25 F-NT2RM4002068//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889.69//Hs.85313:AF071309
 F-NT2RM4002067//ESTs//2.3e-34:455.69//Hs.118273:AA626040
 F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470.61//Hs.162:X16302
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588.61//Hs.122967:AF059569
 30 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532.65//Hs.146459:X66975
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408.62//Hs.69360:U63743
 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202.63//Hs.8152:AB014542
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320.59//Hs.25272:U01877
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388.59//Hs.73858:J05158
 F-NT2RM4002146//ESTs. Highly similar to similar to mago nashi [H.sapiens]/1.6e-135:646.97//Hs.104650:AI037879
 40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763.95//Hs.22464:AF084535
 F-NT2RM4002174
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298.61//Hs.315:L21998
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454.60//Hs.32981:U38276
 45 F-NT2RM4002205//EST//2.6e-21:270.71//Hs.120013:AA707454
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313.61//Hs.118087:AB011182
 F-NT2RM4002226//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //8.4e-125:588.98//Hs.23900:U82984
 50 F-NT2RM4002251//ESTs//1.0:77.74//Hs.155135:AA910966
 F-NT2RM4002256//ESTs//7.5e-28:358.74//Hs.13356:AI205764
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502.57//Hs.77783:AF014118
 F-NT2RM4002278//EST//0.33:138.63//Hs.144096:AI032180
 F-NT2RM4002281
 F-NT2RM4002287//ESTs//0.00037:55.98//Hs.11134:T62979
 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511.72//Hs.31463:D87457
 F-NT2RM4002301
 F-NT2RM4002323//ESTs//3.6e-09:105.87//Hs.131737:AI343331
 F-NT2RM4002339

- F-NT2RM4002344//EST//0.16:166.64//Hs.128600:AA906454
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708.98//Hs.26163:AB014549
- 5 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303.63//Hs.23741:AB018263
 F-NT2RM4002383//ESTs//8.0e-16:153.78//Hs.155243:N70293
 F-NT2RM4002390
 F-NT2RM4002398
 F-NT2RM4002409
- 10 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282.96//Hs.26676:AA033997
 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339.60//Hs.18686:AF052151
 F-NT2RM4002452
 F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228.81//Hs.115263:D30783
 F-NT2RM4002460//EST//1.0:142.65//Hs.145370:AI252780
- 15 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777.98//Hs.8765:AF083255
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464.97//Hs.94781:AB014591
 F-NT2RM4002493
- 20 F-NT2RM4002498//ESTs//1.3e-44:653.67//Hs.23790:N99347
 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225.83//Hs.155464:AF088219
 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290.60//Hs.154968:U02020
 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232.61//Hs.82042:D87075
- 25 F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100.70//Hs.159483:AF054176
 F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393.61//Hs.6619:U84004
 F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226.60//Hs.84043:D84273
- 30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484.93//Hs.105837:AA536054
 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetyltransferase [H.sapiens]//0.059:121.70//Hs.155413:AA429394
 F-NT2RM4002593//ESTs//1.0e-15:103.95//Hs.108920:W28151
- 35 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499.59//Hs.79357:D78275
 F-NT2RM4002623//ESTs//1.2e-11:92.92//Hs.164046:T97402
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746.81//Hs.3628:AB014587
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747.96//Hs.159597:AJ012449
- 40 F-NT2RP1000040//ESTs//1.3e-58:338.92//Hs.17534:H16907
 F-NT2RP1000063//ESTs//0.0013:72.83//Hs.108196:W81647
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548.91//Hs.79971:X98834
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247.61//Hs.30792:AF044924
- 45 F-NT2RP1000111
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324.81//Hs.2052:M86699
 F-NT2RP1000124//ESTs//2.4e-42:268.89//Hs.146078:AI084025
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382.94//Hs.127842:W38901
- 50 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77.90//Hs.3760:AF011792
 F-NT2RP1000170//EST//0.68:130.63//Hs.146994:AI184430
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679.97//Hs.78019:AF070535
 F-NT2RP1000191//ESTs//1.3e-71:405.93//Hs.24054:N46499
- 55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591.58//Hs.74019:X83703
 F-NT2RP1000243
 F-NT2RP1000259
 F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528.97//Hs.

- 4214:AF067730
 F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
- 5 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
 F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204
 F-NT2RP1000357
- 10 F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594
 F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
- 15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159
 F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.3e-177:857:97//Hs.6823:W18181
 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815
- 20 F-NT2RP1000439//EST//0.99:339:56//Hs.137377:AA101603
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862
 F-NT2RP1000460
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985
- 25 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
 F-NT2RP1000493
- 30 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992
 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein mp24//1.9e-06:337:63//Hs.75914:X92098
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418
- 35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475
- 40 F-NT2RP1000630
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576
 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
- 45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612
 F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:A138045
- 50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434
 F-NT2RP1000746
 F-NT2RP1000767
- 55 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023
 F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat//

2.7e-23;147.91//Hs.102336:Z83838

F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143.424:96//Hs.18953:AF067223

F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903

F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990

F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838

F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875

F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094

F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683

F-NT2RP1000915//ESTs//8.1e-11:102:81//Hs.163740:AI248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435

F-NT2RP1001011

F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150

F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523

F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094

F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231

F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724

F-NT2RP1001294

F-NT2RP1001302

F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341

F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815

F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770

F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-
rus]//6.8e-101:480:94//Hs.75017:AA166853

F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859

F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673

F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081

F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
 F-NT2RP1001466
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
 F-NT2RP1001482
 F-NT2RP1001494
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277
 F-NT2RP1001569
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913
 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C. elegans]//8.2e-47:300:89//Hs.6473:AA853955
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390
 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290
 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749
 F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134
 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609
 F-NT2RP2000076//H.sapiens mRNA for TFIIIA/0.00023:356:62//Hs.121686:D14887
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338
 F-NT2RP2000091
 F-NT2RP2000097
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177
 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-158:559:60//Hs.152936:D63475
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
 F-NT2RP2000208

- F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243.61//Hs.143641:AB009462
- F-NT2RP2000232//EST//0.0087:187.62//Hs.151024:Z39990
- F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342.59//Hs.8546:U97669
- 5 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227.60//Hs.47822:AB002378
- F-NT2RP2000248//EST//0.49:117.70//Hs.61016:AA019719
- F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227.60//Hs.30223:X90846
- F-NT2RP2000258//ESTs//3.1e-48:261.94//Hs.128230:AA972691
- 10 F-NT2RP2000270//ESTs//2.9e-38:357.75//Hs.140329:AA714011
- F-NT2RP2000274//ESTs//1.1e-106:508.98//Hs.47646:AA307599
- F-NT2RP2000283//EST//1.0:139.63//Hs.128256:AA972910
- F-NT2RP2000288
- F-NT2RP2000289
- 15 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744.70//Hs.37138:U35376
- F-NT2RP2000298//ESTs//3.1e-46:322.85//Hs.159490:AI123467
- F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381
- F-NT2RP2000327//ESTs//4.3e-18:108.98//Hs.126212:AI417006
- 20 F-NT2RP2000328//ESTs//6.3e-88:437.96//Hs.127336:AI332905
- F-NT2RP2000329//GTP.AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607.66//Hs.101642:X60673
- F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126.69//Hs.153706:AF026547
- F-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981
- 25 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464.57//Hs.12259:AB014530
- F-NT2RP2000412//ESTs//1.0:214.60//Hs.91226:AA649047
- F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375.93//Hs.808:L28010
- F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413.92//Hs.36779:AA626790
- 30 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265
- F-NT2RP2000438//ESTs//1.3e-05:50.98//Hs.156532:AA913381
- F-NT2RP2000448//EST//1.1e-24:136.98//Hs.160402:AI393918
- 35 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158.87//Hs.154655:Z68747
- F-NT2RP2000498//ESTs//1.0e-17:181.79//Hs.155243:N70293
- F-NT2RP2000503//ESTs//4.5e-41:205.100//Hs.62751:AA765702
- F-NT2RP2000510
- F-NT2RP2000516
- 40 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus]//3.2e-15:167.75//Hs.10984:AA806768
- F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196.98//Hs.14409:AB011144
- F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242.57//Hs.114001:Z20656
- 45 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732.97//Hs.7314:AB014514
- F-NT2RP2000644//ESTs//0.035:276.60//Hs.43660:N33174
- F-NT2RP2000656
- F-NT2RP2000658//ESTs//0.032:281.59//Hs.124853:AA420602
- F-NT2RP2000668
- 50 F-NT2RP2000678//ESTs//2.9e-16:310.65//Hs.126867:AI093453
- F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233.78//Hs.114905:AA088442
- F-NT2RP2000710
- F-NT2RP2000715
- 55 F-NT2RP2000731
- F-NT2RP2000758//EST//1.0e-14:199.71//Hs.162409:AA573242
- F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445.89//Hs.21421:AA911739

F-NT2RP2000809//ESTs//1.2e-36;235.89//Hs.154580:N34101
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351.58//Hs.159275:AF030880
 F-NT2RP2000814
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182
 5 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390.70//Hs.20695:AB002292
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167.94//Hs.75794:U80811
 F-NT2RP2000845//ESTs//1.0e-83:403.98//Hs.156828:AI336850
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207.92//Hs.135235:AI081880
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732.94//Hs.3615:AB018284
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189.65//Hs.46146:AA418097
 15 F-NT2RP2000931//MATRIN3//1.1e-130:610.98//Hs.78825:AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326.97//Hs.15144:AC005014
 F-NT2RP2000938//ESTs//1.8e-28:296.75//Hs.22822:H06408
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533.98//Hs.19822:AB018298
 20 F-NT2RP2000965//ESTs//5.3e-59:328.94//Hs.35575:R96494
 F-NT2RP2000970
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385.96//Hs.21875:AA243700
 25 F-NT2RP2000987//ESTs//5.6e-11:177.72//Hs.15776:T91944
 F-NT2RP2001036//ESTs//2.0e-55:352.88//Hs.122131:AA789292
 F-NT2RP2001044//EST//0.069:267.60//Hs.102808:N67117
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696.97//Hs.67619:AB007957
 30 F-NT2RP2001065
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
 F-NT2RP2001081
 F-NT2RP2001094//ESTs//0.0071:262.64//Hs.128115:AI356560
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311.78//Hs.155464:AF088219
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519.63//Hs.80358:U52191
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201.91//Hs.118470:AI336362
 F-NT2RP2001149//EST//3.9e-27:244.78//Hs.162236:AA551582
 F-NT2RP2001168//ESTs//0.0023:216.62//Hs.134938:AI091361
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567.96//Hs.26247:AB007949
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
 F-NT2RP2001196
 F-NT2RP2001218//ESTs//1.1e-65:337.96//Hs.115710:AA524598
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395.59//Hs.2685:Z50053
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656.70//Hs.69740:U09367
 F-NT2RP2001245//EST//0.018:228.62//Hs.116798:AA633813
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
 F-NT2RP2001277//EST//0.42:127.66//Hs.42834:N20277
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527.76//Hs.75848:U39412
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359.71//Hs.76090:M80783
 F-NT2RP2001328//ESTs//5.2e-103:532.94//Hs.69476:AA628522
 55 F-NT2RP2001347//ESTs//4.3e-28:217.82//Hs.31775:H41883
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418.91//Hs.107039:W27244
 F-NT2RP2001378
 F-NT2RP2001381//ESTs//0.59:235.62//Hs.118569:AI377558

- F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:225:62//Hs.159402:AC005609
- F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
- F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
- F-NT2RP2001420
- F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H. sapiens]//0.030:443:59//Hs.140506:AA308018
- F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
- F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
- F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248
- F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218
- F-NT2RP2001449
- F-NT2RP2001450
- F-NT2RP2001467
- F-NT2RP2001506
- F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C. elegans]//3.2e-83:409:98//Hs.156161:AI333779
- F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:Y14494
- F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134
- F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586
- F-NT2RP2001560
- F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957
- F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389
- F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876
- F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268
- F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
- F-NT2RP2001613
- F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229
- F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067
- F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718
- F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328
- F-NT2RP2001675//X-LINKED HELICASE III//0.040:454:58//Hs.96264:U72936
- F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314
- F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:U52840
- F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091
- F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:AI197870
- F-NT2RP2001721
- F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991
- F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697
- F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF091754
- F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180
- F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250
- F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610
- F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219
- F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768
- F-NT2RP2001883
- F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.142189:M74161

- F-NT2RP2001900//EST//1.9e-14:132.84//Hs.130049:AA902650
 F-NT2RP2001907//ESTs. Weakly similar to ankryrin 3, long form [H.sapiens]/0.37:263.62//Hs.106377:H29757
 F-NT2RP2001926//ESTs//1.1e-87:430.97//Hs.133487:AI393754
 F-NT2RP2001936
 5 F-NT2RP2001943
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
 F-NT2RP2001947
 F-NT2RP2001969//ESTs//3.3e-93:433.93//Hs.9622:W44489
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238.63//Hs.155174:AB007892
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235.62//Hs.129943:AB011117
 F-NT2RP2001991//EST//0.0027:163.68//Hs.162458:AA579196
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314.97//Hs.116604:AB018299
 15 F-NT2RP2002032
 F-NT2RP2002033//EST//1.2e-16:224.74//Hs.150409:AI003543
 F-NT2RP2002041//EST//0.022:139.69//Hs.127219:AA939336
 F-NT2RP2002046//ESTs//1.1e-35:218.92//Hs.130678:R51509
 F-NT2RP2002047//ESTs//0.43:131.64//Hs.153939:AI284198
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137.71//Hs.3615:AB018284
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634
 F-NT2RP2002070//ESTs//0.00027:107.72//Hs.4852:R84241
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643.96//Hs.11039:AF052183
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
 F-NT2RP2002079//ESTs//6.2e-06:326.60//Hs.134202:AI313156
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533.97//Hs.155218:AJ007509
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408.60//Hs.122755:AF032986
 30 F-NT2RP2002124//ESTs//1.3e-90:459.96//Hs.142053:AA224286
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319.59//Hs.995:M83363
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112
 F-NT2RP2002172//EST//4.4e-14:276.67//Hs.148392:AI085314
 35 F-NT2RP2002185//ESTs. Weakly similar to ubiquitin S6(1) [D.melanogaster]/6.8e-61:354.91//Hs.109966:C06057
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194.97//Hs.91728:M58460
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASX-alpha mRNA, complete cds//6.8e-15:228.67//Hs.111323:AF077954
 40 F-NT2RP2002208
 F-NT2RP2002219//ESTs//0.0059:247.61//Hs.36495:AA151628
 F-NT2RP2002231//ESTs//0.29:167.63//Hs.112013:AI394318
 F-NT2RP2002235//H.sapiens mRNA for PHAP12b protein//0.86:67.82//Hs.84264:U70439
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264.59//Hs.129748:AB011099
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315.89//Hs.150595:AF005418
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343.71//Hs.92137:M19720
 F-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]/1.3e-31:206.88//Hs.4029:Z78373
 50 F-NT2RP2002292//ESTs//1.3e-07:153.67//Hs.13533:H23079
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467.96//Hs.24812:AF069532
 F-NT2RP2002316//ESTs//0.95:194.63//Hs.157214:AA805445
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594
 55 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257.60//Hs.75516:X54637
 F-NT2RP2002373
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

- 97//Hs.109051:AF038958
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289
 F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098
 5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326
 F-NT2RP2002442//ESTs. Weakly similar to similar to molybdopter biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045
 10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289
 F-NT2RP2002498
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044
 15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212
 F-NT2RP2002537
 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096
 20 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503
 25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805
 F-NT2RP2002621
 30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493
 F-NT2RP2002701//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385
 35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572
 F-NT2RP2002727
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217
 40 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329
 F-NT2RP2002752//EST//1.2e-06:126:74//Hs.159913:AA862709
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705
 45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407
 F-NT2RP2002800
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142
 50 F-NT2RP2002862
 F-NT2RP2002880
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392
 55 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517
 F-NT2RP2002939
 F-NT2RP2002954

- F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:135.91//Hs.108332:U39317
- F-NT2RP2002979
- F-NT2RP2002980
- 5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272.61//Hs.122967:AF059569
- F-NT2RP2002987//ESTs//8.2e-20:99.82//Hs.138965:AI004740
- F-NT2RP2002993
- F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353.81//Hs.155464:AF088219
- 10 F-NT2RP2003034//ESTs//1.6e-08:263.66//Hs.164048:AA811741
- F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019
- F-NT2RP2003099//TRICHOHYALIN//0.98:183.62//Hs.82276:L09190
- F-NT2RP2003108//H. sapiens nek2 mRNA for protein kinase//0.025:185.67//Hs.153704:U11050
- 15 F-NT2RP2003034//ESTs//1.6e-08:263.66//Hs.164048:AA811741
- F-NT2RP2003121//ESTs//1.9e-13:158.73//Hs.129998:AI291379
- F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556.57//Hs.155321:J03161
- F-NT2RP2003129//ESTs//0.095:218.63//Hs.70836:AA121544
- 20 F-NT2RP2003137
- F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227.61//Hs.105958:AB014520
- F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581.93//Hs.9736:D67025
- F-NT2RP2003161//ESTs//0.0095:120.65//Hs.163532:AI424170
- 25 F-NT2RP2003164//EST//0.11:179.63//Hs.163299:AA853944
- F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342.79//Hs.153014:AB002353
- F-NT2RP2003177//ESTs//3.6e-80:414.96//Hs.4767:N91123
- F-NT2RP2003194//ESTs//5.4e-20:119.95//Hs.149531:AI393223
- F-NT2RP2003206//EST//0.095:182.60//Hs.88461:AA278594
- 30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726.93//Hs.154443:X74794
- F-NT2RP2003230//ESTs//3.0e-10:239.62//Hs.163720:AA526947
- F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543.77//Hs.108966:U48696
- 35 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200.62//Hs.102732:U88153
- F-NT2RP2003265
- F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313.93//Hs.109966:C06057
- F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714.96//Hs.154919:AB014525
- 40 F-NT2RP2003280
- F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243.65//Hs.21862:AB011159
- F-NT2RP2003293//ESTs//5.5e-28:418.70//Hs.146227:AI269334
- 45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meiding protein, complete cds//2.0e-86:416.97//Hs.7943:AB006572
- F-NT2RP2003297//EST//0.99:240.60//Hs.133228:AI052312
- F-NT2RP2003307//ESTs//5.6e-15:137.81//Hs.90020:AA442752
- F-NT2RP2003308
- 50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532.95//Hs.6092:T75227
- F-NT2RP2003339//ESTs//0.13:166.63//Hs.149649:AI346765
- F-NT2RP2003347//ESTs//0.96:185.59//Hs.125003:H85963
- F-NT2RP2003367//Human HsLIM15 mRNA for HsLIM15, complete cds//0.99:243.60//Hs.37181:D64108
- 55 F-NT2RP2003391
- F-NT2RP2003393
- F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416.57//Hs.4976:AF039023
- F-NT2RP2003401

- F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/3.7e-33.303.77//Hs.14038:R06800
 F-NT2RP2003445//EST//1.7e-06:154.65//Hs.142843:R36893
 F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273.61//Hs.159360:L22647
 5 F-NT2RP2003456//EST//0.17:95.65//Hs.147190:AI193320
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53.339.78//Hs.132874:AC004770
 F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154.66//Hs.74451:X04106
 10 F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481.60//Hs.80220:U96136
 F-NT2RP2003506
 F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189.62//Hs.107164:M96803
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403.94//Hs.78482:Y16270
 F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)/1.3e-24:151.95//Hs.1976:M12783
 15 F-NT2RP2003522//Zinc finger protein 148 (pH-Z-52)//1.1e-17:512.60//Hs.112180:AF039019
 F-NT2RP2003533//ESTs//1.8e-76:373.98//Hs.140402:AI138765
 F-NT2RP2003543//ESTs//9.3e-65:363.92//Hs.70643:AA030010
 F-NT2RP2003559//ESTs//0.00037:93.77//Hs.157564:AI356513
 20 F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800
 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541.98//Hs.129937:AB007931
 F-NT2RP2003581//EST//1.0:59.76//Hs.158575:AI368947
 F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]/1.3e-63:224.95//Hs.34627:AA126463
 25 F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585.98//Hs.58488:U97067
 F-NT2RP2003629//ESTs//2.0e-103:535.95//Hs.105633:AA479166
 F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216.61//Hs.89591:M97252
 30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371.80//Hs.125231:AF068006
 F-NT2RP2003687//EST//2.9e-14:134.80//Hs.132635:AI032875
 F-NT2RP2003691//ESTs//8.2e-47:296.83//Hs.138852:AA284247
 F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190.61//Hs.18366:L09561
 35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]/5.1e-44:269.91//Hs.139757:N95271
 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518.98//Hs.78494:AB011097
 F-NT2RP2003713
 F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252.83//Hs.86371:AF054180
 40 F-NT2RP2003727//EST//0.52:277.59//Hs.69507:AA111879
 F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:584.71//Hs.118797:U39318
 F-NT2RP2003751
 45 F-NT2RP2003760
 F-NT2RP2003764
 F-NT2RP2003769
 F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247.59//Hs.96055:U47677
 F-NT2RP2003777
 50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]/3.7e-63:356.92//Hs.16131:AA568689
 F-NT2RP2003793//ESTs//4.8e-68:392.92//Hs.93949:AA782955
 F-NT2RP2003825//ESTs//7.6e-79:232.98//Hs.14347:AA287742
 F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300.59//Hs.77768:X63368
 F-NT2RP2003857//EST//1.0:112.62//Hs.139216:AA244425
 55 F-NT2RP2003859
 F-NT2RP2003871//ESTs//2.5e-44:222.99//Hs.146295:AA935780
 F-NT2RP2003885
 F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emmericella nidulans]/2.2e-

- 113.632:92//Hs.50072:AI378221
 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]/1.0:146:67//Hs.156920:AA489296
- 5 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458
 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
 F-NT2RP2003984
- 10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036
 F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]/7.0e-104:556:93//Hs.111081:AI380378
 F-NT2RP2004014
- 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
 F-NT2RP2004042
 F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
- 20 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
 F-NT2RP2004142
- 25 F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]/1.7e-16:276:67//Hs.36779:AA626790
- 30 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
 F-NT2RP2004196
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
 F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]/1.8e-80:386:98//Hs.68791:AA527270
- 35 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]/8.2e-51:474:74//Hs.108990:N25951
- 40 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
- 45 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
- 50 F-NT2RP2004365
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986
 F-NT2RP2004373
 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]/3.3e-97:477:98//Hs.30490:AA146916
- 55 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from Tq21//1.4e-174:875:95//Hs.152759:AC005164
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]/1.2e-92:519:91//Hs.13275:AI341468

- F-NT2RP2004400//EST//0.018:150.65//Hs.158739:AI375367
F-NT2RP2004412
F-NT2RP2004425//EST//0.049:145.64//Hs.160759:R36944
F-NT2RP2004463//ESTs//1.5e-40:207.98//Hs.98057:C15687
5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//0.45:208.61//Hs.24040:AF006823
F-NT2RP2004490
F-NT2RP2004512//ESTs//0.0012:330.61//Hs.70258:AI091203
F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270.79//
10 Hs.73614:U83460
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687.96//Hs.129908:AB011163
F-NT2RP2004551//ESTs//0.0075:285.62//Hs.149442:AI346891
F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291.61//Hs.132206:
15 AF039694
F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334.82//Hs.155464:AF088219
F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136.64//Hs.28020:AB018309
F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104.68//Hs.125729:N99898
F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260.60//Hs.24756:U43895
20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:273.93//Hs.12845:N28835
F-NT2RP2004614//EST//0.99:103.68//Hs.148738:AI224908
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496.98//Hs.5198:AJ006291
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728.98//Hs.29956:
25 AB007929
F-NT2RP2004675//EST//0.65:151.62//Hs.130504:AI003839
F-NT2RP2004681
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327.94//Hs.154919:
AB014525
30 F-NT2RP2004709//ESTs//2.2e-05:98.77//Hs.161898:AA286942
F-NT2RP2004710//ESTs//0.0035:76.82//Hs.108470:R93780
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582.96//Hs.4236:
AB007947
F-NT2RP2004743//EST//0.11:170.64//Hs.112670:AA069242
35 F-NT2RP2004767//EST//1.5e-09:303.65//Hs.148374:AA948183
F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//
3.7e-110:548.96//Hs.85768:W16504
F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547.57//Hs.
107474:AF045451
40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121.64//Hs.2864:
L40157
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
4.9e-118:594.95//Hs.40820:AF058953
F-NT2RP2004802//ESTs//5.6e-16:116.91//Hs.153841:N36043
45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495.97//Hs.67052:
AF054179
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519.83//Hs.84775:M23161
F-NT2RP2004861//ESTs//6.7e-89:427.98//Hs.132980:AI290258
F-NT2RP2004897//ESTs//6.4e-81:431.94//Hs.130961:N79111
50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418.95//Hs.25619:AB007144
F-NT2RP2004936
F-NT2RP2004959
F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456.66//Hs.70617:D31763
F-NT2RP2004962//EST//2.8e-15:242.69//Hs.146794:AI149478
F-NT2RP2004967//ESTs//0.0022:218.63//Hs.131987:AI239735
55 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218.61//Hs.7414:AB007927
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260.60//Hs.
41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478
 F-NT2RP2004999
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//
 Hs.124161:AF065164
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:
 AB014515
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:
 15 AF055917
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:
 AB014564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.
 20 100555:X98743
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:
 AF045583
 25 F-NT2RP2005147
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:A1357582
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:A1357868
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:
 AJ007509
 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
 F-NT2RP2005254//H.sapiens mRNA for PHAP12b protein//1.0:101:71//Hs.84264:U70439
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.
 81452:AF030555
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:A1383932
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//
 Hs.27007:AF060219
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:
 AB014576
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.
 45 1569:U11701
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
 cds//0.016:353:62//Hs.113265:AF032387
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:
 489:96//Hs.107254:AC005943
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.
 113252:U80761
 55 F-NT2RP2005407
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

- F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-
rus]/8.5e-48:295:90//Hs.75017:AA166853
- F-NT2RP2005464//ESTs/2.0e-99:495:96//Hs.3530:AA808243
- 5 F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog/0.032:176:64//Hs.16:D10656
- F-NT2RP2005472//ESTs/1.4e-34:180:98//Hs.158892:AD78412
- F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds/9.9e-48:432:77//Hs.15519:
AB018315
- F-NT2RP2005490//ESTs/4.5e-19:165:84//Hs.134382:AA083573
- F-NT2RP2005491
- 10 F-NT2RP2005495//ESTs/5.6e-96:452:99//Hs.145417:AI084164
- F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds/4.4e-48:621:68//Hs.6833:AB002324
- F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds/1.6e-63:503:78//Hs.7688:
M64930
- F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds/0.56:139:66//Hs.8546:U97669
- 15 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)/1.0:
291:59//Hs.89709:L35546
- F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds/1.2e-82:
444:92//Hs.119023:AF092563
- F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds/2.2e-19:112:99//Hs.6232:
AB018307
- 20 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]/3.5e-50:366:83//Hs.
61833:AA036735
- F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)/9.4e-155:747:97//Hs.159597:
AJ012449
- 25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds/1.9e-131:618:98//Hs.62515:
AB007963
- F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME
III [C.elegans]/2.5e-51:292:93//Hs.105684:H24407
- F-NT2RP2005555//EST/0.046:308:57//Hs.145962:AI276822
- 30 F-NT2RP200557//ESTs/4.6e-48:382:79//Hs.125014:AI422839
- F-NT2RP2005581//ESTs/6.3e-28:166:93//Hs.87803:AA034436
- F-NT2RP2005600//ESTs/1.6e-40:228:93//Hs.160085:AI218627
- F-NT2RP2005605//ESTs/5.7e-13:115:86//Hs.37718:H60071
- F-NT2RP2005620//Homo sapiens epsilon 2b mRNA, complete cds/3.1e-92:447:97//Hs.22396:AF062085
- 35 F-NT2RP2005622//ESTs/0.16:242:63//Hs.136395:AA523702
- F-NT2RP2005635
- F-NT2RP2005637//ESTs/0.055:96:69//Hs.105998:R90905
- F-NT2RP2005640//ESTs/4.5e-16:107:92//Hs.150823:AI292145
- F-NT2RP2005645//ESTs/2.7e-29:181:90//Hs.121653:AI375440
- 40 F-NT2RP2005651//Oxysterol binding protein/0.00011:122:69//Hs.1433065:M86917
- F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds/1.5e-08:351:62//Hs.91400:
AB006626
- F-NT2RP2005669//ESTs/0.016:185:64//Hs.97713:AA442239
- F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds/7.7e-96:462:98//
Hs.25664:AF089814
- 45 F-NT2RP2005683//ESTs/0.83:242:62//Hs.136395:AA523702
- F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE/2.5e-11:328:61//Hs.79217:M77836
- F-NT2RP2005694
- F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds/0.15:496:
55//Hs.79326:L76703
- 50 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds/5.1e-126:599:97//Hs.61638:
AB018342
- F-NT2RP2005719//ESTs/0.58:326:60//Hs.157209:N57527
- F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)/8.2e-46:415:77//Hs.69740:U09367
- 55 F-NT2RP2005723//ESTs/1.0e-15:141:81//Hs.163747:AA174017
- F-NT2RP2005726//EST/3.4e-15:96:95//Hs.156170:AI334191
- F-NT2RP2005732//ESTs/0.99:162:62//Hs.154914:AA721086
- F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and/0.80:362:58//Hs.97220:U96769

F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//
 Hs.159651:AF068868
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.
 26285:AF082516
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:
 Z50115
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.
 34853:U28368
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820
 F-NT2RP2005812
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595
 F-NT2RP2005835
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//
 Hs.59829:AB014602
 F-NT2RP2005853
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:
 98//Hs.50758:AF092564
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567
 F-NT2RP2005868
 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:
 L16782
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399
 F-NT2RP2005933//ESTs. Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:
 AA292186
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339
 F-NT2RP2006023
 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416
 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
 F-NT2RP2006100
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
 F-NT2RP2006166
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:
 AB014554
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:
 AB018315
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503
 F-NT2RP2006219//H.sapiens mRNA for DGC6R protein//4.4e-118:618:93//Hs.153910:X96484
 F-NT2RP2006237
 F-NT2RP2006238
 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:
 60//Hs.75111:D87258

- F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262
F-NT2RP2006320//ESTs. Moderately similar to maternal transcript Maid [M.musculus]/1.9e-29:151:100//Hs.36794:AI038407
- 5 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371
F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974
- F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174
F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
- 10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
- 15 F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266
F-NT2RP2006467
F-NT2RP2006472
F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
- 20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
- 25 F-NT2RP2006573
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)/1.9e-137:637:98//Hs.6764:AJ011972
- 30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560
F-NT2RP3000047
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
- 35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
F-NT2RP3000068
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
F-NT2RP3000085//Propionyl-CoA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608
- 40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164
- 45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
F-NT2RP3000207
- 50 F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
- 55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
F-NT2RP3000252
F-NT2RP3000255
F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

- F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214.67//Hs.80261:L43821
- F-NT2RP3000312//ESTs//2.6e-50:255.97//Hs.146263:AA255863
- 5 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236.63//Hs.102732:U88153
- F-NT2RP3000324//ESTs//3.8e-10:102.83//Hs.55495:AI091242
- F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189.65//Hs.46146:AA418097
- 10 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442.78//Hs.40100:AB002390
- F-NT2RP3000348
- F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164.59//Hs.78582:X80754
- F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649.66//Hs.101642:X60673
- 15 F-NT2RP3000361//ESTs//2.6e-112:531.98//Hs.17672:AA305921
- F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596.95//Hs.21094:AI337016
- F-NT2RP3000393//ESTs//2.6e-18:137.89//Hs.115600:AA351639
- F-NT2RP3000397//ESTs//8.7e-44:355.73//Hs.121961:AA777873
- F-NT2RP3000403//Homo sapiens fomin binding protein 21 mRNA, complete cds//1.6e-175:841.97//Hs.28307:AF071185
- 20 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610.65//Hs.23094:M19503
- F-NT2RP3000433//ESTs//1.5e-32:246.69//Hs.120892:AA724948
- F-NT2RP3000439//Adenosine A2b receptor//0.44:210.62//Hs.45743:X68487
- F-NT2RP3000441
- 25 F-NT2RP3000449//ESTs//0.60:177.64//Hs.132605:AI051562
- F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315.58//Hs.75562:U48705
- F-NT2RP3000456//ESTs//7.5e-23:140.92//Hs.5209:AA780068
- F-NT2RP3000484//EST//2.5e-06:166.67//Hs.149950:AI289822
- F-NT2RP3000487//ESTs//1.2e-63:311.98//Hs.143304:AI084058
- 30 F-NT2RP3000512//Homo box B3//3.1e-18:109.97//Hs.49931:X16667
- F-NT2RP3000526//ESTs//3.7e-74:424.93//Hs.42991:N21379
- F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706.63//Hs.79347:D86966
- F-NT2RP3000531//ESTs//9.6e-75:392.95//Hs.144148:H08308
- F-NT2RP3000542//ESTs//3.2e-88:448.96//Hs.30622:AA486412
- 35 F-NT2RP3000561//EST//0.88:92.64//Hs.148290:AA908404
- F-NT2RP3000562//ESTs//1.1e-112:522.99//Hs.125153:AA453723
- F-NT2RP3000578
- F-NT2RP3000582//ESTs//2.1e-82:413.97//Hs.118544:R17277
- F-NT2RP3000584
- 40 F-NT2RP3000590//ESTs//1.0:134.64//Hs.12969:N56904
- F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502.57//Hs.77234:AB001914
- F-NT2RP3000596//ESTs//6.8e-71:361.95//Hs.118741:AA179811
- F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355.92//Hs.114622:AA693492
- F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553.59//Hs.79170:D86980
- 45 F-NT2RP3000605//ESTs//5.8e-51:283.94//Hs.127152:AI421203
- F-NT2RP3000622//ESTs//1.7e-10:72.98//Hs.155360:AA984683
- F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194.61//Hs.79386:X54162
- F-NT2RP3000628//ESTs//0.96:221.61//Hs.131161:AI017333
- F-NT2RP3000632//ESTs//4.4e-53:244.77//Hs.143010:AA767904
- 50 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343.84//Hs.155464:AF088219
- F-NT2RP3000661
- F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305.59//Hs.13063:AF017789
- F-NT2RP3000685
- 55 F-NT2RP3000690//EST//1.0:149.64//Hs.140263:AA709001
- F-NT2RP3000736//ESTs//5.3e-26:146.97//Hs.98613:D83884
- F-NT2RP3000739//ESTs//0.0046:66.87//Hs.6880:V26854
- F-NT2RP3000742//ESTs//5.5e-08:311.61//Hs.152224:AI369426

- F-NT2RP3000753//ESTs//2.6e-63:318.97//Hs.153000:AA777765
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245.91//Hs.2427:D89937
 F-NT2RP3000815
 5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
 F-NT2RP3000826//Homo sapiens *delfx* (Dx) mRNA, complete cds//0.00040:263.65//Hs.124024:AF053700
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363.96//Hs.23803:AA126476
 F-NT2RP3000841//EST//0.36:224.60//Hs.162094:AA524012
 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593.68//Hs.157199:X97630
 F-NT2RP3000847//ESTs//0.0028:56.92//Hs.116406:AA209520
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323.86//Hs.155464:AF088219
 F-NT2RP3000852
 15 F-NT2RP3000859//ESTs//0.39:169.62//Hs.148948:AA699918
 F-NT2RP3000865//EST//0.15:236.62//Hs.123366:AA811476
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766.60//Hs.15432:U53445
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701.60//Hs.79706:U53204
 20 F-NT2RP3000875
 F-NT2RP3000901//ESTs//8.2e-26:191.87//Hs.18793:R99101
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374
 F-NT2RP3000917
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340.60//Hs.108985:X68277
 25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351.83//Hs.2953:X84407
 F-NT2RP3000980//ESTs//6.5e-10:102.81//Hs.86950:AI204212
 F-NT2RP3000994//ESTs//4.1e-120:571.98//Hs.127295:AA918411
 F-NT2RP3001004//ESTs//1.1e-76:438.88//Hs.144554:N92198
 F-NT2RP3001007
 30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588.98//Hs.128781:AA160707
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282.97//Hs.30303:AI244662
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534.74//Hs.27007:AF060219
 35 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474.60//Hs.21264:AB018325
 F-NT2RP3001098//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428.60//Hs.155481:AJ006470
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712.64//Hs.82292:D86969
 40 F-NT2RP3001109//ESTs//1.2e-67:323.99//Hs.134734:AI337050
 F-NT2RP3001111
 F-NT2RP3001113//EST//1.1e-33:173.99//Hs.112640:AA609088
 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023
 F-NT2RP3001116//ESTs//1.1e-15:93.98//Hs.58412:W74779
 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258.61//Hs.12107:AF042384
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687.75//Hs.69740:U09367
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341.60//Hs.94790:AB018318
 F-NT2RP3001133//Homo sapiens box A4//0.00011:484.59//Hs.77637:M74297
 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851.98//Hs.5378:AB018305
 F-NT2RP3001147
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257.59//Hs.957:M84605
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891.98//Hs.72160:AJ006266
 F-NT2RP3001176
 55 F-NT2RP3001214//EST//0.88:218.60//Hs.161147:AI417859
 F-NT2RP3001216//ESTs//1.5e-66:340.96//Hs.105994:W19981
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512.95//Hs.103816:AA130866
 F-NT2RP3001232//EST//0.0016:116.71//Hs.136498:AA594010

- F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132
 F-NT2RP3001253//Human preproimatinin mRNA, complete cds//0.99:293:60//Hs.32934:U27109
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:54//Hs.107809:AB018269
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
 10 F-NT2RP3001274
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060
 15 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920
 20 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
 F-NT2RP3001384//Homo sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:99//Hs.146214:AB015332
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
 F-NT2RP3001426
 F-NT2RP3001427
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397
 40 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393
 F-NT2RP3001447
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323
 F-NT2RP3001459
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:AF072836
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI199074
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

- F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Cq class)//0.049:185:65//Hs.1686:M69013
 5 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/9.6e-51:345:82//Hs.144563:AF057280
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435
 F-NT2RP3001629
 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173
 F-NT2RP3001646
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012449
 15 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]/9.0e-53:375:85//Hs.41127:AA555184
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]/4.0e-111:518:99//Hs.20364:AI420022
 20 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.melanogaster]/1.4e-31:191:94//Hs.131279:AA486291
 25 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]/1.7e-159:747:98//Hs.6823:W18181
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177
 30 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [*Caenorhabditis elegans*]/3.5e-116:554:98//Hs.144332:AA046836
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918
 F-NT2RP3001739
 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:U27193
 40 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:AB007928
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
 45 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:U68727
 50 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [*C.elegans*]/2.9e-94:452:98//Hs.54952:AA872675
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326
 55 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
 F-NT2RP3001928//ESTs//7.4e-16:141:82//Hs.138852:AA284247
 F-NT2RP3001931

- F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398
F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:
AB014575
- 5 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
F-NT2RP3001969
F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219
F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779
F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
- 10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153
F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:
AA993745
F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155
F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:
407:97//Hs.131888:AI091806
- 15 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503
F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710
F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//
0.91:194:65//Hs.1298:J03779
- 20 F-NT2RP3002081
F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:
297:61//Hs.102732:U88153
F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256
F-NT2RP3002108
- 25 F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018
F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260
F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with
some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative
CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009
- 30 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644
F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985
F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]
//3.0e-61:340:93//Hs.11379:AA594140
- 35 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046
F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME
III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915
F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643
F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic)//0.98:
242:57//Hs.114001:Z20656
- 40 F-NT2RP3002248
F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261
F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.
110637:AC004080
- 45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139
F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386
F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910
F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871
F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383
- 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:
588:75//Hs.154672:X16396
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:
Y16355
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397.Z70200
F-NT2RP3002399
- 55 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:
AB014578

- F-NT2RP3002484//ESTs//0.95:166.63//Hs.149993:AI291310
 F-NT2RP3002501//ESTs//0.92:43.90//Hs.119314:AA432108
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173.61//Hs.81234:AB007935
 5 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763.93//Hs.57738:U35246
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833.98//Hs.19542:AB018272
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510.70//Hs.96759:AA469984
 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226.62//Hs.12068:X78706
 F-NT2RP3002587//EST//4.8e-31:330.74//Hs.139415:AA426054
 F-NT2RP3002590//EST//1.3e-40:202.100//Hs.144716:AI187919
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280.63//Hs.89631:U48508
 F-NT2RP3002603
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264.61//Hs.3845:AB014888
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320.58//Hs.121287:AF029900
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441.63//Hs.155481:AJ006470
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615.58//Hs.151518:U38847
 20 F-NT2RP3002660//ESTs//2.9e-32:164.100//Hs.152982:AA584308
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493.70//Hs.41086:AI337400
 F-NT2RP3002671//ESTs//3.7e-05:288.59//Hs.161359:AI421991
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294.100//Hs.128750:AI367584
 F-NT2RP3002687
 F-NT2RP3002688//EST//1.0:312.58//Hs.156800:AI352200
 F-NT2RP3002701//EST//0.00083:55.87//Hs.159750:AI393657
 F-NT2RP3002713//ESTs//0.93:229.61//Hs.150459:AI279514
 30 F-NT2RP3002763//ESTs//1.7e-97:419.96//Hs.121593:W86291
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161.62//Hs.129736:AF040753
 F-NT2RP3002785
 F-NT2RP3002799//EST//1.7e-17:199.73//Hs.118694:AA148713
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423.93//Hs.41068:AA844350
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615.70//Hs.105940:AF004715
 F-NT2RP3002861//ESTs//1.1e-88:468.94//Hs.159821:AA524070
 F-NT2RP3002869//ESTs//3.4e-23:132.97//Hs.148873:T33582
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557.88//Hs.123090:AB001895
 F-NT2RP3002877//ESTs//1.1e-19:160.84//Hs.118273:AA626040
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853.98//Hs.6162:AB018314
 F-NT2RP3002911//ESTs//2.8e-07:160.70//Hs.140402:AI138765
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645.97//Hs.3826:U69560
 45 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594.57//Hs.74599:AB011160
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412.57//Hs.21198:AB018262
 F-NT2RP3002969//EST//3.7e-50:272.94//Hs.162331:AA563870
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361.75//Hs.8003:AC004997
 F-NT2RP3002978//ESTs//2.8e-46:253.95//Hs.151924:AI287703
 F-NT2RP3002985//Human TFIIIB related factor hBRF (hBRF) mRNA, complete cds//0.071:550.58//Hs.32935:U28838
 F-NT2RP3002988//EST//0.0016:180.63//Hs.147632:AI218308
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201.63//Hs.72925:M91083
 F-NT2RP3003032//ESTs//9.1e-40:241.92//Hs.113363:C06446
 F-NT2RP3003059//ESTs//0.0015:399.58//Hs.136895:AA897749
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633.59//Hs.1242:X16609

- F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
 F-NT2RP3003078
 F-NT2RP3003101
- 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740
 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
- 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
 F-NT2RP3003150
 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
- 15 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
- 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497
- 25 F-NT2RP3003242//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460
 F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
- 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947
- 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
 F-NT2RP3003330
 F-NT2RP3003344
- 40 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791
- 45 F-NT2RP3003385//ESTs. Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653
 F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942
- 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268
- 55 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169
 F-NT2RP3003552
 F-NT2RP3003555/ESTs//1.4e-12:81.98//Hs.144487:AI418322
 F-NT2RP3003564/EST//4.5e-08:186.69//Hs.116769:AA630365
 5 F-NT2RP3003572/EST//0.27:105.69//Hs.162134:AA526311
 F-NT2RP3003576/ESTs//1.2e-57:277.84//Hs.138852:AA284247
 F-NT2RP3003589/RAS-RELATED PROTEIN RAB-8//6.3e-38:373.73//Hs.123109:X56741
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564.61//Hs.104:
 D14012
 10 F-NT2RP3003625
 F-NT2RP3003656
 F-NT2RP3003659
 F-NT2RP3003665/ESTs//0.015:221.62//Hs.153705:AA527586
 F-NT2RP3003672/ESTs//0.70:351.57//Hs.27633:N78184
 15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:
 63//Hs.44585:U58334
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246.62//Hs.118463:AF055000
 F-NT2RP3003701/EST//0.93:79.69//Hs.145285:AI249848
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478.61//Hs.48998:AB007865
 20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700.98//Hs.48513:
 AB018300
 F-NT2RP3003746
 F-NT2RP3003795/ESTs//7.1e-20:228.74//Hs.159571:AA454230
 F-NT2RP3003799
 25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432.73//Hs.1422:
 M19722
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:
 242.57//Hs.114001:Z20656
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//
 5.1e-07:624.59//Hs.96028:AF042832
 30 F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171.63//Hs.
 102877:U41315
 F-NT2RP3003825
 F-NT2RP3003828/ESTs//2.1e-12:434.61//Hs.156864:AI346481
 35 F-NT2RP3003831
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242.98//Hs.25300:
 AF070611
 F-NT2RP3003842//Integrin, beta 8//1.0:345.60//Hs.832:M73780
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335.68//Hs.26450:AB018268
 40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805.99//Hs.118738:
 AB018343
 F-NT2RP3003876/ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243.90//Hs.124832:AA846576
 F-NT2RP3003914/ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
 PRECURSOR [D.melanogaster]//1.1e-107:499.99//Hs.105794:AA701659
 45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:
 404.77//Hs.9006:AF057358
 F-NT2RP3003932/ESTs//0.94:278.58//Hs.15661:W02396
 F-NT2RP3003989/ESTs//1.0:174.64//Hs.8095:AI359006
 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433.58//Hs.
 50 93909:AF042498
 F-NT2RP3004013/ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617.97//Hs.
 142151:AA984061
 F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283.62//Hs.
 155302:U57317
 55 F-NT2RP3004041/EST//0.98:264.58//Hs.127552:AA953234
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774.67//Hs.26441:AB002317
 F-NT2RP3004070/EST//6.8e-22:163.85//Hs.132635:AI032875
 F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520.90//Hs.

- 100007:X76091
F-NT2RP3004093
F-NT2RP3004095/Human clone 23732 mRNA, partial cds/3.3e-27:372.69//Hs.81281:U97258
F-NT2RP3004110/Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211.77//Hs.40100:AB002390
5 F-NT2RP3004125/ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF.7.1 [Xenopus laevis]/1.0e-126:590.99//Hs.129888:AI096509
F-NT2RP3004145
F-NT2RP3004148
F-NT2RP3004155/Homo sapiens timing protein CLK-1 mRNA, complete cds/2.1e-121:578.98//Hs.157113:
10 AF032900
F-NT2RP3004189/ESTs//1.3e-80:409.97//Hs.151001:AA564706
F-NT2RP3004206/Human mRNA for stac, complete cds//1.0:245.60//Hs.56045:D86640
F-NT2RP3004207/Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)/0.095:281:
62//Hs.101047:M31523
15 F-NT2RP3004209/ESTs//5.8e-87:458.94//Hs.155303:AI221835
F-NT2RP3004215/ESTs//0.074:56.80//Hs.163590:H43361
F-NT2RP3004242
F-NT2RP3004246/EST//0.20:219.63//Hs.161920:AA483240
F-NT2RP3004253/ESTs//1.2e-36:204.96//Hs.143588:AI149140
20 F-NT2RP3004258/Human gene for neurofilament subunit M (NF-M)/7.2e-07:369.59//Hs.71346:Y00067
F-NT2RP3004262/Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733.98//Hs.
158471:AF088982
F-NT2RP3004282/Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597.61//Hs.19261:AF007871
F-NT2RP3004332
25 F-NT2RP3004334/ESTs//8.8e-27:142.99//Hs.28068:H06285
F-NT2RP3004341/EST//0.0068:213.64//Hs.153208:X96426
F-NT2RP3004348/ESTs//1.2e-18:126.93//Hs.58595:AA830999
F-NT2RP3004349/ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME
III [Caenorhabditis elegans]/3.9e-45:337.83//Hs.141429:AA631915
30 F-NT2RP3004378/ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]/
4.3e-125:608.98//Hs.128781:AA160707
F-NT2RP3004399/H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804.90//Hs.123122:
X97249
F-NT2RP3004424/ESTs, Weakly similar to JTV-1 [H.sapiens]/3.2e-122:609.96//Hs.20132:AA203113
35 F-NT2RP3004428/Homo sapiens ALR mRNA, complete cds//0.00044:458.60//Hs.153638:AF010403
F-NT2RP3004451/Bone morphogenetic protein 8 (osteogenic protein 2)/0.00023:357.59//Hs.99948:M97016
F-NT2RP3004454/Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583.99//Hs.27349:
AB007917
F-NT2RP3004466/Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399.58//Hs.22616:AB014564
40 F-NT2RP3004470/EST//1.3e-56:331.91//Hs.136830:AA769219
F-NT2RP3004472
F-NT2RP3004475/Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715.98//Hs.5003:AB007925
F-NT2RP3004480/ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]/
4.6e-116:547.99//Hs.124768:AA307735
45 F-NT2RP3004490/Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752.97//Hs.158311:AB012851
F-NT2RP3004498/ESTs, Moderately similar to ROSA26AS [M.musculus]/3.5e-89:425.99//Hs.126082:AI077718
F-NT2RP3004503/EST//5.3e-49:399.81//Hs.162335:AA564256
F-NT2RP3004504/Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370.59//Hs.158244:AB007948
F-NT2RP3004507/Human zinc finger protein (MAZ) mRNA//0.86:129.66//Hs.7647:M94046
50 F-NT2RP3004527/EST//0.053:260.62//Hs.123314:AA810110
F-NT2RP3004534/ESTs//3.5e-78:370.99//Hs.132808:AI031571
F-NT2RP3004539/Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679.98//Hs.75970:
AB014532
F-NT2RP3004544/Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793.98//Hs.74750:
55 AB011126
F-NT2RP3004566/ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]/2.2e-66:362.94//Hs.
125870:AI364967
F-NT2RP3004569

- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181.860.97//
Hs.122752:AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422.97//Hs.129928:
AB007923
- 5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796.95//Hs.72160:AJ006266
- F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356.64//
Hs.124138:AI266336
- F-NT2RP3004618//ESTs//1.5e-42:481.70//Hs.130768:AA909232
- 10 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538.56//Hs.79706:U53204
- F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
- F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827.98//
Hs.118991:AA675919
- F-NT2RP4000023//ESTs//1.4e-33:182.96//Hs.122722:AA455668
- F-NT2RP4000035//ESTs//1.1e-23:283.72//Hs.142147:AA706495
- 15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556.85//Hs.129844:AF029761
- F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441.62//Hs.155481:
AJ006470
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720.97//Hs.159597:
AJ012449
- 20 F-NT2RP4000102//ESTs//8.8e-33:184.82//Hs.93054:H47743
- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774.99//Hs.57929:AB011538
- F-NT2RP4000111
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548.98//Hs.64691:
AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212.63//Hs.75520:D26069
- F-NT2RP4000150
- F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431.59//Hs.3386:AF053356
- F-NT2RP4000159
- F-NT2RP4000167
- 30 F-NT2RP4000185//ESTs//1.1e-51:240.68//Hs.33020:N31946
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825.98//Hs.13999:
AB014600
- F-NT2RP4000212//ESTs//1.6e-10:74.95//Hs.111885:AA422006
- F-NT2RP4000214//ESTs//3.9e-11:225.68//Hs.59793:AA451731
- 35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425.71//Hs.
46468:U45984
- F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771.97//Hs.155481:
AJ006470
- F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:
384.89//Hs.115498:AA436298
- 40 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604.99//Hs.43728:
AF091092
- F-NT2RP4000263
- F-NT2RP4000290//EST//1.0:149.63//Hs.136928:AA812580
- 45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685.63//Hs.158132:D63481
- F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547.57//Hs.
143648:AB000732
- F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589.58//Hs.83634:U52112
- F-NT2RP4000355
- 50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654.99//Hs.107479:
AB018281
- F-NT2RP4000367//Homo sapiens ikappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-
137:649.97//Hs.31323:AF044195
- F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECUR-
SOR [S.cerevisiae]//1.2e-09:157.76//Hs.97950:AI382073
- 55 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//
0.098:291.59//Hs.994:M95678
- F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509.59//Hs.929:M57965

- F-NT2RP4000398//Zinc finger protein 140 (clone PHZ-39)//4.9e-60:469:68//Hs.154205:U09368
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
- 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:A1249468
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
- 10 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995
- 15 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
 F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840
- 20 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372
 F-NT2RP4000524
 F-NT2RP4000528
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:A1348154
- 25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730
- 30 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907
- 35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.11817:T80622
- 40 F-NT2RP4000785//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
- 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
- 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278
 F-NT2RP4000865//Zinc finger protein 136 (clone PHZ-20)//2.0e-96:415:78//Hs.69740:U09367
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:A1206803
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
- 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901
 F-NT2RP4000918
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

- F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//
 Hs.24812:AF069532
- 5 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371
 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
 F-NT2RP4000979
 F-NT2RP4000984
- 10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U09013
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204
 F-NT2RP4001004
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
- 15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.
 113287:AF009204
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:
 L40157
- 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:
 AJ006470
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
 F-NT2RP4001079//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//1.4e-131:634:98//Hs.
 106778:AJ010953
- 25 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.
 146459:X66975
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164
 F-NT2RP4001095
- 30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis
 familiaris]//2.2e-26:171:92//Hs.14038:R06800
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.6e-37:185:
 100//Hs.126925:AA931237
- 35 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476286
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
- 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
 F-NT2RP4001207
- 45 F-NT2RP4001210//ESTs//3.1e-95:480:97//Hs.46913:AI017636
 F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.
 122967:AF059569
- 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463
 F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//
 Hs.31121:U40571
- 55 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578
 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
 mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

- F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110
 F-NT2RP4001339
 F-NT2RP4001343
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625
 5 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
 F-NT2RP4001372
 10 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101.Z50194
 F-NT2RP4001375
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918
 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933
 F-NT2RP4001442
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326
 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997
 20 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.63220:AA522707
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395
 25 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
 F-NT2RP4001567
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
 F-NT2RP4001574
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228
 F-NT2RP4001592
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
 40 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
 F-NT2RP4001634
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
 45 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
 50 F-NT2RP4001696
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522

- F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
- F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
- 5 F-NT2RP4001823//Human facio-genital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690
- F-NT2RP4001828
- F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
- F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
- 10 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572
- F-NT2RP4001861//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
- F-NT2RP4001889
- 15 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from T2p21/4.4e-108:535:97//Hs.15144:AC005014
- F-NT2RP4001896
- F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
- F-NT2RP4001927
- F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442
- 20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
- F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
- F-NT2RP4001953//ESTs//0.018:208:65//Hs.130105:AA904868
- F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047
- 25 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560
- 30 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139
- F-NT2RP4002052
- F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873
- F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999
- 35 F-NT2RP4002075
- F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104
- F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654
- F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684
- 40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284
- F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204
- F-NT2RP4002888
- F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
- F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995
- 45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
- F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067
- F-NT2RP5003492
- F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179
- 50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131
- F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542
- F-NT2RP5003522
- F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943
- 55 F-NT2RP5003534
- F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934
- F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

- F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairnia moschata]/4.4e-75:355:99//Hs.36727: A1051983
- F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
- F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922
- 5 F-OVARC1000017//Homo sapiens mRNA for NTA, complete cds//0.50:482:58//Hs.113264:AB005060
- F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603
- F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
- F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]/6.7e-60:305:97//Hs.31696: H50008
- 10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
- F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
- F-OVARC1000085
- F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
- F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778
- 15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
- F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]/2.9e-73:406:92//Hs.109463:Al205174
- F-OVARC1000109
- F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
- 20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401: AB011134
- F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:Al384010
- F-OVARC1000139
- F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
- 25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
- F-OVARC1000151
- F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
- F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)/0.10:504:59//Hs.154083:U70136
- 30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:Al249131
- F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
- F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
- F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens] //2.7e-31:264:79//Hs.151895:AA196379
- 35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
- F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]/0.00084:170:65//Hs.107747:Al357868
- F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
- F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
- F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]/0.51:193:66//Hs.6194:Al378579
- 40 F-OVARC1000321
- F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60// Hs.122359:AF051946
- F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
- 45 F-OVARC1000347
- F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450
- F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930
- F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA581862
- 50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
- F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930
- F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]/1.7e-25:190:84//Hs.139513:AA259082
- F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
- F-OVARC1000437//Filamin 1 (actin-binding protein-280)/0.93:281:60//Hs.76279:X53416
- 55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284
- F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:Al377423
- F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334: AB014583

- F-OVARC1000461//ESTs//1.0e-39:215.95//Hs.131532:AI024524
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252.58//Hs.108112:AF070640
 F-OVARC1000466//ESTs//3.6e-14:189.71//Hs.164041:R51854
 F-OVARC1000473//ESTs//0.00012:77.85//Hs.29173:AA134926
 5 F-OVARC1000479
 F-OVARC1000486//ESTs//4.2e-07:409.60//Hs.99280:AA453036
 F-OVARC1000496//ESTs//6.0e-14:240.69//Hs.131900:AI023327
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539.99//Hs.111285:AF051850
 F-OVARC1000526//ESTs//2.9e-08:368.611//Hs.42771:N26740
 10 F-OVARC1000533//EST//3.4e-14:137.82//Hs.123405:AA813492
 F-OVARC1000543//ESTs//0.13:278.61//Hs.54894:N98475
 F-OVARC1000556//ESTs//1.4e-31:217.90//Hs.106385:W26667
 F-OVARC1000557//ESTs//3.8e-20:208.76//Hs.138919:AA827410
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:
 15 66//Hs.85302:U76421
 F-OVARC1000573//ESTs//2.1e-22:268.76//Hs.121852:AA776358
 F-OVARC1000576//ESTs//9.4e-22:124.98//Hs.24220:W22200
 F-OVARC1000578//EST//4.7e-31:335.74//Hs.162881:AA652729
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263.63//Hs.3080:U29725
 20 F-OVARC1000605//EST//0.1:148.62//Hs.163346:AA883722
 F-OVARC1000622//EST//4.3e-50:313.88//Hs.149580:AI281881
 F-OVARC1000640//ESTs//2.6e-55:441.80//Hs.105319:AA470097
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-
 plete cds//1.6e-78:424.93//Hs.86859:D43772
 25 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536.94//Hs.111862:
 AB011162
 F-OVARC1000678//EST//1.3e-08:131.77//Hs.145970:AI277106
 F-OVARC1000679//ESTs//0.66:223.61//Hs.134782:H74279
 F-OVARC1000681//EST//0.017:315.61//Hs.147799:AI221639
 30 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549.99//Hs.
 125315:AF027156
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479.57//Hs.4764:AB018306
 F-OVARC 1000700
 F-OVARC1000703//ESTs//0.41:100.68//Hs.160699:AI284320
 35 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//
 1.2e-110:451.91//Hs.13476:AF038661
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318.91//Hs.7049:
 AI141736
 F-OVARC1000746//ESTs//3.2e-123:570.99//Hs.127295:AA918411
 40 F-OVARC1000769//ESTs//0.072:177.67//Hs.142573:AA601196
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194.99//
 Hs.157059:W28130
 F-OVARC1000781//ESTs//4.0e-14:113.89//Hs.41972:AA626793
 F-OVARC1000787//EST//0.92:91.64//Hs.163258:AA828835
 45 F-OVARC1000800//ESTs//1.6e-44:193.81//Hs.163971:N27584
 F-OVARC1000802//ESTs//4.6e-43:395.80//Hs.115401:AA400032
 F-OVARC1000834//ESTs//1.9e-91:431.99//Hs.154450:AA069390
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432.100//Hs.155995:
 AB014543
 50 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632.99//Hs.18910:AF045584
 F-OVARC1000862//ESTs, Highly similar to gene Fir protein [M.musculus]//6.1e-31:183.93//Hs.108620:AA418155
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133.69//Hs.
 159234:U89995
 F-OVARC1000883//ESTs//0.44:154.63//Hs.98183:AA471143
 55 F-OVARC1000885//EST//0.91:152.63//Hs.160765:AI313323
 F-OVARC1000886//ESTs//4.6e-08:375.61//Hs.131653:AI025777
 F-OVARC 1000890
 F-OVARC1000891

- F-OVARC1000897//ESTs//1.1e-07:145.69//Hs.119878:AA706818
 F-OVARC1000912//EST//3.6e-08:376.61//Hs.158782:Al376601
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA244556
 5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119
 F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843
 10 F-OVARC 1000948
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:Al088986
 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:Al283069
 15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661
 F-OVARC1000986//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317
 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219
 20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114
 F-OVARC1001004
 F-OVARC1001010
 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866
 F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:Al023584
 25 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:Al050735
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149
 F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:Al168074
 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385
 30 F-OVARC1001051
 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:Al312873
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451
 35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248
 40 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897
 F-OVARC1001107//Homo sapiens SKB1b mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF051782
 45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
 F-OVARC1001118
 F-OVARC1001129
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
 50 F-OVARC1001162
 F-OVARC1001167
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:Al078279
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
 55 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581
 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551
 F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

- C06057
F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.4e-52:324:90//Hs.114673:W72675
F-OVARC1001200//ESTs/3.9e-16:104:94//Hs.125520:AA883889
5 F-OVARC1001232//Cyclin A/0.95:124:67//Hs.85137:X51688
F-OVARC1001240//EST/0.017:351:60//Hs.120655:AA745676
F-OVARC1001243//ESTs/0.78:291:59//Hs.132458:AI424825
F-OVARC1001244//RING3 PROTEIN/2.8e-19:118:95//Hs.75243:D42040
10 F-OVARC1001261//EST/1.9e-42:225:96//Hs.158854:AI377837
F-OVARC1001268//ESTs/0.66:239:61//Hs.132525:AA576821
F-OVARC1001270//ESTs/0.99:204:60//Hs.144647:AA625224
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:AB014543
F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]/0.11:355:60//Hs.108812:AA044835
15 F-OVARC1001296//ESTs/1.1e-46:237:98//Hs.33746:N78172
F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.152455:AF044209
F-OVARC1001329//ESTs/1.4e-97:486:97//Hs.125886:AA884264
F-OVARC1001330
20 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)/0.021:232:62//Hs.79410:U62531
F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]/2.5e-78:363:99//Hs.105837:AA538054
F-OVARC1001342//EST/0.98:97:65//Hs.148210:AA897493
F-OVARC1001344//EST/5.3e-10:241:64//Hs.138777:N67251
25 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715
F-OVARC1001360//ESTs/4.9e-87:429:97//Hs.130145:AI264633
F-OVARC1001369//ESTs/6.3e-07:371:62//Hs.131653:AI025777
F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554
30 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL/4.1e-149:683:99//Hs.151428:AJ224819
35 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242
F-OVARC1001399//ESTs/1.1e-35:264:83//Hs.59379:W28225
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651
F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426
40 F-OVARC1001425//ESTs/2.4e-11:258:67//Hs.119197:T83651
F-OVARC1001436
F-OVARC1001442
F-OVARC1001453
F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]/1.9e-125:581:99//Hs.110950:AI041823
45 F-OVARC1001480//ESTs/0.95:125:72//Hs.152584:AA584568
F-OVARC1001489//EST/4.9e-72:341:100//Hs.148191:AA897343
F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507
50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)/1.1e-97:538:92//Hs.75813.L33243
F-OVARC1001525
F-OVARC1001542//Envoplakin/0.34:258:60//Hs.25482:U53786
F-OVARC1001547//EST/0.0046:237:62//Hs.54638:N90595
F-OVARC1001555
55 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/6.8e-57:275:98//Hs.155160:AF031166
F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/0.0035:271:60//Hs.108465:AI144299

- F-OVARC1001610/ESTs, Weakly similar to F22E10.5 [C.elegans]/1.4e-43:216:99//Hs.120002:AI038398
F-OVARC1001611
F-OVARC1001615/EST/0.99:135:68//Hs.129410:AA993500
F-OVARC1001668/Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144
5 F-OVARC1001702/Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867
F-OVARC1001703/EST//1.7e-24:172:88//Hs.121198:AA757229
F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858
F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
10 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825
F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588
F-OVARC1001762
F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670
15 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575
F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697
F-OVARC1001791
20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
F-OVARC1001802/EST//3.7e-45:254:92//Hs.130620:AI005102
F-OVARC1001805/Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287
F-OVARC1001809/Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172
25 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453
F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
30 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
F-OVARC1001861
F-OVARC1001873/Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611
F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
35 F-OVARC1001880/Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
F-OVARC1001883/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953
F-OVARC1001900/Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749
40 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834
F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
F-OVARC1001916/H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
F-OVARC1001928
45 F-OVARC1001942/Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
F-OVARC1001943/ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794
F-OVARC1001949/KRAB zinc finger protein (alternative products)//1.8e-17:294:67//Hs.22556:U37251
F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776
F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
F-OVARC1002050/Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934
55 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
F-OVARC1002082/EST//2.5e-09:213:67//Hs.112810:AA610063
F-OVARC1002107

- F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174
- F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
- F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022
- 5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
- F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
- F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868
- F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568
- 10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517
- F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
- F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
- F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789
- 15 F-PLACE1000014
- F-PLACE1000031
- F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
- F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
- F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755
- 20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
- F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771
- F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366
- 25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
- F-PLACE1000094
- F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378
- F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135
- 30 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291
- F-PLACE1000185
- F-PLACE1000213
- 35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
- F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
- F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
- F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202
- F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
- 40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
- F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
- F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197
- F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
- 45 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
- F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
- F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260
- 50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
- F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053
- F-PLACE1000424
- F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
- 55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) //2.7e-52:421:80//Hs.69747:M35531
- F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638
- F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

- F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289
- 5 F-PLACE1000562
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542
- 10 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA578571
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
 F-PLACE1000636
- 15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
- 20 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694
- 25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
 F-PLACE1000769
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215
- 30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736
- 35 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201
 F-PLACE1000948
- 40 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h25 [C. elegans]//9.3e-45:309:88//Hs.13531:R61789
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267
- 45 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876
- 50 F-PLACE1001024
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204
 F-PLACE1001062
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859
- 55 F-PLACE1001088
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

- 71//Hs.150406:AF022158
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704
 F-PLACE1001168
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135
 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741
 F-PLACE1001238
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591
 F-PLACE1001351
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342
 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:AF009615
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419
 25 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS6 [H.sapiens]//0.00083:187:64//Hs.5399:N30646
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete CDS//0.0038:496:57//Hs.97681:AJ233333
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452
 30 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529
 F-PLACE1001503
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753
 F-PLACE1001545
 F-PLACE1001551
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
 45 F-PLACE1001602//Human POJ domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
 F-PLACE1001611//Human facio-genital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
 F-PLACE1001640
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

- F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
- F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
- 5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
- F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
- F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
- F-PLACE1001745
- F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
- 10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243
- F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750
- F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
- F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050
- 15 F-PLACE1001781
- F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
- F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
- F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
- 20 3.6e-110:546:96//Hs.40820:AF058953
- F-PLACE1001821
- F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
- F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
- F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
- 25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257
- F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220
- F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936
- F-PLACE1001928//H. sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837
- 30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778
- F-PLACE1001989
- F-PLACE1002004
- F-PLACE1002046
- F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108
- 35 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555
- F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
- F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178
- F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765
- 40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637
- F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831
- F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747
- F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631
- 45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390
- F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891
- F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627
- F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674
- F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U9289
- 50 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989
- F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127862:AI024442
- F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935
- F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503
- F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675
- 55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279
- F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291
- F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710
- F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

- F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458.66//Hs.40993:AF000148
- F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947
- 5 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158
- F-PLACE1002465
- F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369.63//Hs.129361:AJ007581
- F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523
- 10 F-PLACE1002493
- F-PLACE1002499
- F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708.59//Hs.111967:U76010
- F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482
- 15 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583.95//Hs.88756:AB018256
- F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566.96//Hs.99348:AC004774
- F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198.86//Hs.51124:AF019369
- F-PLACE1002571//Homo sapiens mRNA for TP53, complete cds//0.99:274:59//Hs.138202:AF027866
- 20 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627
- F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725
- F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279.74//Hs.109606:D44497
- F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
- 25 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915
- F-PLACE1002625
- F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693.62//Hs.80562:X04412
- F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
- F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804.97//Hs.124903:AF068180
- 30 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509.60//Hs.157091:M13903
- F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
- F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
- 35 F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
- F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
- F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298.62//Hs.26285:AF082516
- F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
- 40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567.70//Hs.77546:D79994
- F-PLACE1002815
- F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687.73//Hs.9028:AF039691
- F-PLACE1002834//ESTs//2.6e-41:393.74//Hs.120206:AI089163
- F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167
- 45 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
- F-PLACE1002853//ESTs//1.1e-20:136.90//Hs.125895:AA889024
- F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
- F-PLACE1002908//ESTs//3.8e-48:325.88//Hs.54702:AI040029
- F-PLACE1002941//ESTs//5.0e-18:128.88//Hs.17376:AA855056
- 50 F-PLACE1002962
- F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815
- F-PLACE1002991
- F-PLACE1002993
- F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104.86//Hs.124808:T86959
- 55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
- F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632.97//Hs.129872:AB011088

- F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567
F-PLACE1003045
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
F-PLACE1003136
F-PLACE1003145
10 F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209
F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
15 F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)/0.99:175:62//Hs.85112:X57025
F-PLACE1003256
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
20 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376
F-PLACE1003334
F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308
25 F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3)mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715
F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]/8.9e-35:332:78//Hs.163820:H71277
30 F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009
F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069
F-PLACE1003383
35 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]/8.9e-113:590:94//Hs.125175:AI142546
F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)/0.40:206:62//Hs.30223:X90846
F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
40 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635
F-PLACE1003516//Human kpn1 repeat mrna (cdna clone pcd-kpn1-8), 3' end//3.4e-85:357:86//Hs.103948:K00627
F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633
45 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
F-PLACE1003537//ESTs, Weakly similar to ZK58.6 [C.elegans]/3.6e-110:543:97//Hs.120416:AA057428
F-PLACE1003553
F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367
50 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
F-PLACE1003592//ESTs, Moderately similar to !!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/1.4e-50:287:93//Hs.154799:AA130620
F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
55 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104

- F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 5 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:A1365413
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 10 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
 15 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
 F-PLACE1003768//Human knpi repeat mna (cdna clone pcd-knpi-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
 F-PLACE1003783
 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
 20 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
 F-PLACE1003823//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
 25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X77770
 F-PLACE1003886
 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
 30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
 35 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
 40 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.153045:X52056
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526
 45 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
 50 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
 55 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

- F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914
- F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830
- 5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
- F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
- F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
- F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588
- F-PLACE1004336
- 10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153
- F-PLACE1004376//ESTs. Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
- F-PLACE1004384//Human HsLIM15 mRNA for HsLIM15, complete cds//2.0e-49:466:76//Hs.37181:D64108
- F-PLACE1004388
- 15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871
- F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
- F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
- F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
- 20 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
- F-PLACE1004460
- F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
- F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
- F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
- 25 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
- F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
- F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
- F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
- 30 F-PLACE1004518
- F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
- F-PLACE1004550//ESTs. Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
- F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
- 35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
- F-PLACE1004645
- F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
- F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
- F-PLACE1004664
- 40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
- F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
- F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
- 45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
- F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
- F-PLACE1004693//ESTs. Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
- F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542
- F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891
- 50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.115993:AA700148
- F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680
- F-PLACE1004743
- F-PLACE1004751//ESTs. Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470
- 55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367
- F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391
- F-PLACE1004793
- F-PLACE1004804

- F-PLACE1004813//EST//2.8e-42:296.83//Hs.155725:AI310340
 F-PLACE1004814//ESTs. Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415.95//Hs.80965:AA493284
- 5 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294.69//Hs.22111:AB002362
 F-PLACE1004824//ESTs//0.0072:128.69//Hs.164062:AA934047
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669
 F-PLACE1004838
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910
- 10 F-PLACE1004868
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
 F-PLACE1004900
 F-PLACE1004902//ESTs//4.7e-72:367.96//Hs.54971:AI424382
 F-PLACE1004913//ESTs//0.031:166.63//Hs.130110:AA904929
- 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402.64//Hs.118910:U82130
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519.88//Hs.17839:AF099936
 F-PLACE1004934//ESTs//7.2e-43:231.78//Hs.133503:AA628592
- 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
 F-PLACE1004969
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235.60//Hs.27610:U34605
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331.83//Hs.153468:AB011147
- 25 F-PLACE1004982//ESTs//0.020:148.63//Hs.129377:AI218520
 F-PLACE1004985//ESTs//7.9e-05:372.61//Hs.87606:AA242831
 F-PLACE1005028//ESTs//4.6e-29:212.89//Hs.137451:AA351459
 F-PLACE1005027//ESTs//6.5e-91:455.97//Hs.30890:H15159
- 30 F-PLACE1005046//ESTs//3.7e-56:250.96//Hs.152730:AI308943
 F-PLACE1005052//EST//1.8e-36:370.73//Hs.123424:AA813594
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761.98//Hs.14687:AB011148
 F-PLACE1005060//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757.56//Hs.122967:AF059569
- 35 F-PLACE1005077//EST//0.79:283.591//Hs.89276:AA283899
 F-PLACE1005085//ESTs//3.5e-18:231.72//Hs.142654:AA324740
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401.80//Hs.153468:AB011147
- 40 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194.80//Hs.75437:1.40401
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538.62//Hs.104640:AF000561
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405.57//Hs.73166:U76366
 F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N83227
- 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291.63//Hs.2557:Y00661
 F-PLACE1005146//ESTs. Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360.63//Hs.142177:H11741
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563.72//Hs.154326:D42087
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259.60//Hs.128316:AB014541
- 50 F-PLACE1005181//ESTs. Weakly similar to No definition line found [C.elegans]//4.4e-126:583.99//Hs.25347:AI138605
 F-PLACE1005187//ESTs//6.2e-34:222.90//Hs.124265:N70417
 F-PLACE1005206//EST//0.089:167.62//Hs.140487:AA767009
- 55 F-PLACE1005232//ESTs. Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192.60//Hs.47334:W2370
 F-PLACE1005243
 F-PLACE1005261//ESTs//0.52:245.58//Hs.6682:T76941

- F-PLACE1005266//Kalimann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182
 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
 5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
 F-PLACE1005313
 10 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
 F-PLACE1005373
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
 15 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503
 20 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
 25 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
 F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261
 30 F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
 F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
 F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
 F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
 35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
 F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
 F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
 F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255
 40 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
 45 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
 F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258
 F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
 50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
 F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
 F-PLACE1005802
 F-PLACE1005803
 55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482

- F-PLACE1005828/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/4.1e-42:
327:81//Hs.138404:R70986
- F-PLACE1005834/Retinoblastoma 1 (including osteosarcoma)/0.038:436:58//Hs.75770:L41870
- F-PLACE1005845/ESTs/4.8e-50:309:89//Hs.107149:AI379497
- 5 F-PLACE1005850/ESTs/7.1e-40:253:79//Hs.158096:AA186905
- F-PLACE1005851/ESTs/7.6e-93:483:95//Hs.135608:AA732242
- F-PLACE1005876/ESTs/0.97:282:60//Hs.98664:AI381487
- F-PLACE1005884/ESTs/0.070:276:60//Hs.106057:AI031552
- F-PLACE1005890/ESTs/1.5e-91:500:93//Hs.136993:AA843300
- 10 F-PLACE1005898
- F-PLACE1005921
- F-PLACE1005923/ESTs/0.50:308:58//Hs.52489:R61504
- F-PLACE1005925/ESTs/0.024:93:68//Hs.149868:AI288274
- F-PLACE1005932/TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR/0.97:342:57//Hs.89839:
M18391
- 15 F-PLACE1005934/ESTs/8.6e-10:74:93//Hs.25092:AA922142
- F-PLACE1005936/DNA excision repair protein ERCC5/1.0:144:63//Hs.48576:X69978
- F-PLACE1005951/B94 PROTEIN/0.00025:371:61//Hs.75522:M92357
- F-PLACE1005953/ESTs/2.8e-06:290:61//Hs.140996:R73468
- 20 F-PLACE1005955/ESTs, Weakly similar to Y53C12A.3 [C.elegans]/0.15:136:66//Hs.107747:AI357868
- F-PLACE1005966/Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:
U13948
- F-PLACE1005968
- F-PLACE1005990
- 25 F-PLACE1006002/Putative mismatch repair/binding protein hMSH3/1.9e-48:312:77//Hs.42674:U61981
- F-PLACE1006003/EST/0.00018:171:67//Hs.138882:W73256
- F-PLACE1006011
- F-PLACE1006017/ESTs/3.1e-21:159:88//Hs.142173:AA757743
- F-PLACE1006037/Homo sapiens mRNA for KIAA0789 protein, complete cds/0.021:202:64//Hs.158319:
AB018332
- 30 F-PLACE1006040/Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906
- F-PLACE1006076/EST/0.29:92:64//Hs.161536:N80395
- F-PLACE1006119/Homo sapiens Ran-GTP binding protein mRNA, partial cds/4.1e-147:679:99//Hs.4976:
AF039023
- 35 F-PLACE1006129
- F-PLACE1006139
- F-PLACE1006143/Human mRNA for KIAA0355 gene, complete cds/9.3e-43:357:79//Hs.153014:AB002353
- F-PLACE1006157/ESTs, Weakly similar to ETX1 (alternatively spliced) [H.sapiens]/2.9e-12:119:84//Hs.23153:
R92857
- 40 F-PLACE1006159/ESTs/2.3e-87:443:96//Hs.23740:H17868
- F-PLACE1006164/ESTs/0.099:223:60//Hs.8108:AA902721
- F-PLACE1006167/Homo sapiens chromosome 19, cosmid F23149/1.1e-68:333:92//Hs.152894:AC005239
- F-PLACE1006170/ESTs/0.081:171:67//Hs.135187:AI074005
- F-PLACE1006187/Homo sapiens cyclin E2 mRNA, complete cds/1.2e-150:694:99//Hs.30464:AF091433
- 45 F-PLACE1006195/ESTs/8.9e-14:229:70//Hs.141470:N49608
- F-PLACE1006196/ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog/3.5e-59:369:88//Hs.
135623:AA134719
- F-PLACE1006205
- F-PLACE1006223/ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]
//0.0089:166:63//Hs.127179:AI279486
- 50 F-PLACE1006225
- F-PLACE1006236/EST/0.060:89:69//Hs.136977:AA830668
- F-PLACE1006239/ESTs/0.028:105:66//Hs.142336:AA358185
- F-PLACE1006246/ESTs/0.060:330:60//Hs.105695:AI085802
- 55 F-PLACE1006248/Homo sapiens mRNA for KIAA0648 protein, partial cds/7.3e-168:791:98//Hs.31921:
AB014548
- F-PLACE1006262
- F-PLACE1006288/Homo sapiens mRNA for Pex3 protein/4.8e-37:186:100//Hs.7277:AJ001625

- F-PLACE1006318
 F-PLACE1006325//ESTs//3.7e-25;206.83//Hs.102319:AI246503
 F-PLACE1006335//ESTs//2.0e-27;161.95//Hs.163529:AI361492
 F-PLACE1006357//ESTs//0.013;268.61//Hs.105775:AA526249
 5 F-PLACE1006360//ESTs//4.8e-27;146.98//Hs.100739:Z98481
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65;272.59//Hs.153529:AF070581
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07;403.61//Hs.105940:AF004715
 F-PLACE1006382//EST//0.98;77.68//Hs.136933:AA814693
 10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111;539.97//Hs.22396:AF062085
 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36;424.74//Hs.21560:AB002296
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111;525.98//Hs.131846:AF069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24;531.65//Hs.101414:AB011129
 15 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0;248.60//Hs.88219:AF060866
 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24;210.62//Hs.89659:AC004381
 F-PLACE1006470
 20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46;520.71//Hs.131953:AF059194
 F-PLACE1006488//ESTs//6.2e-47;239.97//Hs.158161:AA312511
 F-PLACE1006492//ESTs//0.82;37.100//Hs.160417:AA488493
 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98;505.56//Hs.75063:AL023584
 25 F-PLACE1006521//ESTs//0.032;222.63//Hs.23171:AA706542
 F-PLACE1006531//EST//2.1e-53;258.100//Hs.117316:AA699358
 F-PLACE1006534//EST//1.8e-07;78.89//Hs.157551:AI356219
 F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96;383.58//Hs.32963:D31784
 30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058;464.57//Hs.1540:L36529
 F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17;372.65//Hs.17630:AB018280
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168;781.99//Hs.155377:U97670
 35 F-PLACE1006617//ESTs//6.0e-08;354.60//Hs.42624:H99088
 F-PLACE1006628//NUCLEOLIN//0.0044;186.66//Hs.79110:M60858
 F-PLACE1006629//Homo sapiens (clone s22171) mRNA fragment//0.097;229.63//Hs.26956:L40396
 F-PLACE1006640//ESTs//0.00019;380.59//Hs.13672:AI131473
 40 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12;113.83//Hs.3385:N25917
 F-PLACE1006678
 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16;284.60//Hs.153638:AF010403
 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05;382.63//Hs.43627:U35612
 F-PLACE1006754//Biliary glycoprotein//8.9e-27;305.72//Hs.50964:X16354
 45 F-PLACE1006760//ESTs//0.10;207.62//Hs.152589:AA954152
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025;251.64//Hs.89591:M97252
 F-PLACE1006782//ESTs//1.2e-90;423.100//Hs.132826:AI075783
 F-PLACE1006792//ESTs//1.5e-10;439.58//Hs.138501:AI051228
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10;84.95//Hs.123642:M83941
 50 F-PLACE1006800//ESTs//0.00068;360.61//Hs.157876:AI422017
 F-PLACE1006805//ESTs//4.6e-103;491.98//Hs.140465:AA769892
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47;403.56//Hs.15832:AB014518
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103;619.87//Hs.23094:M19503
 55 F-PLACE1006829//ESTs//1.5e-22;141.94//Hs.142988:AA142876
 F-PLACE1006860//EST//0.0062;206.65//Hs.158793:AI376773
 F-PLACE1006867//ESTs//0.068;218.62//Hs.91166:AA551273
 F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0;268.58//Hs.5333:AB018254

- F-PLACE1006883//ESTs//1.6e-75:398.94//Hs.119544:T95601
 F-PLACE1006901//ESTs//1.9e-13:87.96//Hs.134737:AI089187
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
 F-PLACE1006917
- 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127.L12723
 F-PLACE1006961//ESTs. Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67.98//Hs.21806:AA630312
- 10 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
- 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957
- 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)/0.18:268:63//Hs.904:U84010
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
- 25 F-PLACE1007112
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
 F-PLACE1007228//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
- 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
- 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:L06133
 F-PLACE1007282
- 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7 alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//Hs.144877:AF029403
 F-PLACE1007342
- 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:567:98//Hs.76596:AF096870
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642
- 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436
- 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

- F-PLACE1007484//ESTs//7.1e-18:127.91//Hs.100251:AA535975
F-PLACE1007488
- F-PLACE1007507//ESTs//1.2e-99:274.98//Hs.123462:AA903385
F-PLACE1007511//Keratin 19//4.2e-31:586.64//Hs.23761:Y00503
- 5 F-PLACE1007524//ESTs//6.8e-71:356.97//Hs.163067:AA897296
F-PLACE1007525//ESTs//0.073:242.59//Hs.128711:AA856979
F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468.57//Hs.113283:AF018080
F-PLACE1007544//ESTs//1.7e-74:360.98//Hs.128632:AI076755
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733.71//Hs.65238:
- 10 AB014561
F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
F-PLACE1007583//ESTs//1.8e-46:234.98//Hs.155071:AA584257
F-PLACE1007598//ESTs//1.7e-83:400.99//Hs.120206:AI089163
F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778.56//Hs.33010:AB014533
- 15 F-PLACE1007621
F-PLACE1007632//ESTs//1.7e-32:175.97//Hs.122278:AA781867
F-PLACE1007645
F-PLACE1007649
F-PLACE1007677//ESTs//3.0e-13:125.82//Hs.143382:AA476266
- 20 F-PLACE1007688//ESTs//6.8e-06:311.61//Hs.132926:AI027055
F-PLACE1007690//ESTs//1.9e-13:83.98//Hs.150088:AI348503
F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216.63//Hs.1103:X02812
F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637.70//Hs.75789:D87953
F-PLACE1007708//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709.97//Hs.4812:
- 25 AF061243
F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233.89//Hs.108797:
AA476815
F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:
64//Hs.104129:AA923278
- 30 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728.98//Hs.153121:
AB014585
F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364.68//Hs.159347:M62424
F-PLACE1007743//ESTs//0.029:421.58//Hs.106090:AA457030
F-PLACE1007746//ESTs//6.7e-55:330.89//Hs.153392:AI089469
- 35 F-PLACE1007791//EST//0.39:261.62//Hs.145991:AI277656
F-PLACE1007807//ESTs//2.0e-54:385.83//Hs.163930:AA640504
F-PLACE1007810//ESTs//6.1e-53:416.81//Hs.152395:AA533107
F-PLACE1007829//EST//0.28:271.61//Hs.125514:AA883841
F-PLACE1007843//EST//0.020:307.59//Hs.145535:AI261635
- 40 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396.77//Hs.23094:M19503
F-PLACE1007852
F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894.98//Hs.28020:
AB018309
F-PLACE1007868//ESTs//3.0e-50:333.86//Hs.15792:AI038387
- 45 F-PLACE1007877
F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943
F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755.97//Hs.
92381:AB007956
F-PLACE1007946//ESTs//8.9e-16:250.68//Hs.88527:N24002
- 50 F-PLACE1007954//ESTs//1.6e-05:76.90//Hs.63314:AA056538
F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813.98//Hs.
5671:AF084530
F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:
730.98//Hs.78106:AF079529
- 55 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264.92//Hs.42222:
W28567
F-PLACE1007990//ESTs//1.2e-104:493.99//Hs.118445:AI097043
F-PLACE1008000//Homo sapiens vcl1 mRNA, complete cds//5.7e-63:578.74//Hs.150380:AF087693

- F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
 F-PLACE1008044
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
 5 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197
 10 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI216883
 F-PLACE1008177//ESTs. Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135
 15 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
 20 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
 F-PLACE1008273
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129
 30 F-PLACE1008331//ESTs. Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
 35 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171
 F-PLACE1008398
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
 40 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499
 45 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487
 F-PLACE1008437
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901
 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823
 55 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-pter//1.1e-45:507:71//Hs.8003:AC004997
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

- F-PLACE1008584//ESTs//1.4e-13:252.68//Hs.153429:AI283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175.812.98//Hs.23255:AB018334
- 5 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350.66//Hs.151087:AA649326
 F-PLACE1008625//ESTs//0.86:269.57//Hs.94998:N26794
 F-PLACE1008626//ESTs//0.55:69.71//Hs.92096:F10560
 F-PLACE1008627//ESTs//3.0e-62:302.99//Hs.120766:H82458
 F-PLACE1008629//EST//0.0012:174.67//Hs.121195:AA757211
- 10 F-PLACE1008630//ESTs//4.5e-77:371.99//Hs.132960:AA252394
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299.64//Hs.76415:D38535
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135.622.99//Hs.147967:AF044333
 F-PLACE1008693//EST//0.19:36.94//Hs.138817:N93728
- 15 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137.97//Hs.90443:AF038406
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183.63//Hs.119534:AJ224741
 F-PLACE1008748//ESTs//0.88:204.63//Hs.15139:AA527080
- 20 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285.69//Hs.35460:H65503
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503.97//Hs.6458:AF060543
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127.68//Hs.111380:AA258772
 F-PLACE1008807//ESTs//0.81:346.58//Hs.116901:AA663542
- 25 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376.98//Hs.7179:AF011905
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD) [Hs.75668:M81883
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falci-
 ciparum (isolate k1 / thailand)]//0.73:354.59//Hs.26322:AA156858
- 30 F-PLACE1008854//ESTs//3.0e-26:391.66//Hs.133260:AI052728
 F-PLACE1008867//ESTs//5.9e-08:64.93//Hs.91115:AI221563
 F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701.68//Hs.23094:M19503
 F-PLACE1008902//EST//0.85:425.60//Hs.140573:AA826323
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753.98//Hs.62318:AB018308
- 35 F-PLACE1008925//ESTs//0.025:133.67//Hs.103218:W84771
 F-PLACE1008934//ESTs//0.27:307.59//Hs.135168:AI394026
 F-PLACE1008941//ESTs//3.3e-53:266.98//Hs.108677:AA488937
 F-PLACE1008947//Human TBP-associated factor (HTAFII130) mRNA, partial cds//2.4e-13:625.58//Hs.24644:U75308
- 40 F-PLACE1009020//ESTs//3.3e-11:122.81//Hs.131777:AI024950
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763.96//Hs.34780:AJ003112
 F-PLACE1009039//EST//0.76:111.63//Hs.160997:H55762
 F-PLACE1009045//ESTs//2.2e-76:399.95//Hs.114919:AA457689
- 45 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93.100//Hs.119689:S70585
 F-PLACE1009050//ESTs//1.4e-92:451.98//Hs.66373:AI239698
 F-PLACE1009060//ESTs//1.4e-14:86.100//Hs.131725:AI090525
 F-PLACE1009090//ESTs//2.7e-20:198.78//Hs.110044:AA181800
- 50 F-PLACE1009091//ESTs//0.99:342.57//Hs.46903:AI093091
 F-PLACE1009094//ESTs//1.0:225.63//Hs.120374:AI337031
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733.74//Hs.104020:X68011
 F-PLACE1009110//ESTs//2.6e-91:453.96//Hs.143756:AI040890
 F-PLACE1009111//ESTs//2.7e-15:159.77//Hs.146811:AA410788
- 55 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671.97//Hs.99742:AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718.59//Hs.35804:D25215
 F-PLACE1009150//Human HsLIM15 mRNA for HsLIM15, complete cds//1.7e-50:440.78//Hs.37181:D64108

- F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440.69//Hs.158095:AB007953
- F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245.61//Hs.92614:M62302
- 5 F-PLACE1009166//EST//0.98:114.67//Hs.137706:AA977250
- F-PLACE1009172//EST//6.2e-34:267.64//Hs.161081:N22770
- F-PLACE1009174//ESTs//6.0e-24:234.77//Hs.155196:AI282821
- F-PLACE1009183//EST//0.021:261.62//Hs.144222:N90100
- 10 F-PLACE1009186//ESTs. Weakly similar to No definition line found [C.elegans]//3.6e-117:588.95//Hs.54943:Z78396
- F-PLACE1009190//EST//0.046:95.70//Hs.131646:AI025689
- F-PLACE1009200//EST//2.5e-41:195.78//Hs.162404:AA573131
- F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157.77//Hs.146403:M29540
- F-PLACE1009248//EST//0.13:178.62//Hs.23298:R22575
- 15 F-PLACE1009298//ESTs. Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121.98//Hs.124768:AA307735
- F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195.62//Hs.148101:M88338
- F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411.59//Hs.23731:U83192
- 20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594.86//Hs.23094:M19503
- F-PLACE1009335//EST//0.037:169.63//Hs.148875:AI240767
- F-PLACE1009338//ESTs//5.7e-22:123.98//Hs.66783:AA059473
- F-PLACE1009368
- F-PLACE1009375
- 25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317.81//Hs.43681:AL022394
- F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730.74//Hs.9450:M27878
- F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207.61//Hs.101174:AF047863
- F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210.86//Hs.3404:AF035262
- F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599.68//Hs.155291:D13630
- 30 F-PLACE1009443//H. sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350.58//Hs.82128:AJ012159
- F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146.93//Hs.76987:AF012872
- F-PLACE1009459//H. sapiens gap gene mRNA, complete CDS//1.0:241.60//Hs.151641:Z24680
- F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4, 5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347.60//Hs.994:M95678
- 35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67AI//4.1e-91:464.96//Hs.155049:AC004531
- F-PLACE1009477//ESTs//0.30:221.61//Hs.107287:AI308839
- F-PLACE1009493//Homo sapiens mRNA for LAK-4p. complete cds//1.6e-30:608.63//Hs.16165:AB002405
- F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526.78//Hs.8517:U07028
- 40 F-PLACE1009539//ESTs//3.3e-18:186.83//Hs.71922:AA148417
- F-PLACE1009542//EST//7.8e-11:265.65//Hs.159692:AI416956
- F-PLACE1009571//ESTs//6.1e-15:94.97//Hs.151458:AA600866
- F-PLACE1009581//Microtubule-associated protein 1A//1.0:196.59//Hs.147918:U38291
- F-PLACE1009595//EST//1.8e-28:179.92//Hs.60090:AA004806
- 45 F-PLACE1009596//ESTs. Weakly similar to LIS-1 protein [H. sapiens]//4.1e-16:281.66//Hs.13889:AI341394
- F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313.79//Hs.113283:AF018080
- F-PLACE1009613//ESTs//0.50:297.60//Hs.25114:AI074011
- F-PLACE1009621//ESTs//1.4e-98:470.98//Hs.124695:AI094085
- F-PLACE1009622//ESTs//9.8e-14:94.93//Hs.117227:AA682773
- 50 F-PLACE1009637//ESTs//4.9e-92:440.98//Hs.126587:AA917087
- F-PLACE1009639
- F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816.98//Hs.21862:AB011159
- F-PLACE1009665//ESTs//9.1e-45:383.79//Hs.61199:AA024494
- 55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701.98//Hs.109590:AF062534
- F-PLACE1009708//ESTs. Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S. cerevisiae]//7.5e-51:295.92//Hs.48541:AA827926
- F-PLACE1009721//EST//0.18:467.58//Hs.124358:AA830650

- F-PLACE1009731//ESTs//1.0.207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-
 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-
 130:600:95//Hs.16411:AL030996
 F-PLACE1009845
 F-PLACE1009861
 F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021
 F-PLACE1009886
 F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889
 F-PLACE1009908
 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379
 F-PLACE1009925
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446
 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:
 AB014529
 F-PLACE1010023
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.
 142151:AA984061
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:
 AF065482
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus
 musculus]//1.8e-38:212:95//Hs.98067:AA236822
 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:
 U69567
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:
 AF020761
 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.
 122967:AF059569
 F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682
 F-PLACE1010134//H.sapiens hbrn mRNA//1.2e-14:380:64//Hs.77590:X72889
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740
 F-PLACE1010152
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582
 F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:
 H69637
 F-PLACE1010231
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:
 AB007917
 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590
 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540
 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813
 F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248
 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

- F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855
 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648
 5 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
 F-PLACE1010401
 F-PLACE1010481//Human BLU protein (BLU) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
 15 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
 F-PLACE1010580//ESTs. Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete
 20 cds//9.9e-148:707:97//Hs.19851:AF045186
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200
 25 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
 F-PLACE1010662
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
 F-PLACE1010743//Human myosin-IxB mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
 F-PLACE1010761//ESTs. Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
 40 F-PLACE1010771//ESTs. Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNPG [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
 F-PLACE1010786
 F-PLACE1010800
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
 F-PLACE1010833//ESTs. Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.132736:AA583494
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
 F-PLACE1010857//ESTs. Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.130135:AA905493
 50 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
 F-PLACE1010900
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
 F-PLACE1010917

- F-PLACE1010925//ESTs//2.6e-81:437.94//Hs.5876:H26537
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653.98//Hs.74750:AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437.98//Hs.66392:AF064244
- 5 F-PLACE1010944//ESTs//1.3e-17:117.91//Hs.29444:W30985
 F-PLACE1010947//EST//0.97:93.72//Hs.162299:AA555154
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444.59//Hs.585:X04506
- 10 F-PLACE1010960//ESTs//0.98:238.60//Hs.163674:AA506632
 F-PLACE1010965//ESTs//3.1e-74:376.96//Hs.115679:AI379721
 F-PLACE1011026//EST//0.022:222.60//Hs.47154:N50931
 F-PLACE1011032//EST//1.1e-05:88.79//Hs.118024:N34032
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179.67//Hs.1177:U10886
- 15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207.68//Hs.994:M95678
 F-PLACE1011054//H. sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310.78//Hs.2407:Z49194
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228.61//Hs.153640:U56998
- 20 F-PLACE1011057//EST//2.5e-80:388.98//Hs.126466:AA913320
 F-PLACE1011090//ESTs//1.4e-94:469.97//Hs.106448:R76663
 F-PLACE1011109//ESTs//0.13:303.62//Hs.49294:AA418037
 F-PLACE1011114//ESTs//5.8e-12:75.100//Hs.147422:AI214317
 F-PLACE1011133//ESTs//0.17:225.62//Hs.132853:AI370857
- 25 F-PLACE1011143//ESTs//0.013:264.63//Hs.115368:AA629949
 F-PLACE1011160
 F-PLACE1011165//Galactokinase 2//2.7e-32:194.92//Hs.129228:M84443
 F-PLACE1011185//EST//1.4e-34:261.83//Hs.140250:AA708114
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-124:576.99//Hs.159140:AF038664
- 30 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469.99//Hs.8241:AA283057
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221.88//Hs.101821:W27452
 F-PLACE1011221//ESTs//0.46:238.62//Hs.32853:AA015751
- 35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675.99//Hs.23168:AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350.98//Hs.15144:AC005014
 F-PLACE1011273//ESTs//1.0:222.59//Hs.35274:AA495803
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191.65//Hs.140950:AF070637
- 40 F-PLACE1011296//ESTs//0.019:137.63//Hs.140654:AA865915
 F-PLACE1011310//EST//0.066:336.58//Hs.162529:AA584160
 F-PLACE1011325//ESTs//7.4e-43:229.96//Hs.21081:H08310
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696.99//Hs.5819:AF102265
- 45 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120.81//Hs.159897:AB007970
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684.63//Hs.76415:D38535
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325.99//Hs.107245:AA627053
- 50 F-PLACE1011399//ESTs//8.6e-05:285.61//Hs.130105:AA904868
 F-PLACE1011419//ESTs//0.70:240.62//Hs.159650:N95552
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743.98//Hs.10801:AB011102
- 55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557.72//Hs.23094:M19503
 F-PLACE1011465//EST//3.1e-58:380.85//Hs.131605:AI025204
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703.99//Hs.111138:AB018255

- F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482
- F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264
- F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997
- 5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319
- F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476
- F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333
- F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180
- 10 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462
- F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778
- F-PLACE1011641
- F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631
- 15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661
- F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086
- F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745
- F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
- F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234
- 20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366
- F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350
- F-PLACE1011725
- F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853
- F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891
- 25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240
- F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693
- F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660
- F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664
- F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
- 30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152
- F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
- F-PLACE1011896//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868
- F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
- F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
- 35 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
- F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
- F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591
- F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
- 40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256
- F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
- F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503
- 45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
- F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
- F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831
- F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
- F-PLACE2000017
- 50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557
- F-PLACE2000030
- F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
- F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
- 55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
- F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
- F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
- F-PLACE2000061

- F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
 5 F-PLACE2000100
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:U56417
 F-PLACE2000115
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
 F-PLACE2000132
 F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
 15 F-PLACE2000164
 F-PLACE2000170
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179
 F-PLACE2000176
 F-PLACE2000187
 20 F-PLACE2000216
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958
 25 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
 F-PLACE2000317
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299
 F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 45 F-PLACE2000411
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080
 F-PLACE2000455//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082
 55 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

- F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128
 F-PLACE3000029
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445
 10 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
 F-PLACE3000121
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
 F-PLACE3000148
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147
 F-PLACE3000160
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
 F-PLACE3000194
 F-PLACE3000197
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
 35 F-PLACE3000226
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
 40 F-PLACE3000244
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
 F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
 F-PLACE3000310
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586
 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
 50 F-PLACE3000331
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
 F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
 55 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

- F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441
F-PLACE3000363
F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
F-PLACE3000399//Clathrin, light polypeptide (Lcb)/5.2e-70:391:81//Hs.73919:X81637
F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715
10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:
116:78//Hs.77579:AF013263
F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]/1.6e-51:260:98//Hs.122512:
H61502
15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:
AB018344
F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:
183:93//Hs.108326:AB006202
20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
F-PLACE4000009//TRICHOHYALIN/3.1e-09:692:60//Hs.82276:L09190
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:
AB018352
25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:
AC004131
F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.
40993:AF000148
30 F-PLACE4000063
F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:
35 AB007931
F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
F-PLACE4000129
F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
F-PLACE4000192
F-PLACE4000211
F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317
F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
F-PLACE4000261
F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]/9.5e-41:202:
100//Hs.118849:AA215645
F-PLACE4000270
55 F-PLACE4000300
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

- F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292
 F-PLACE4000367
 F-PLACE4000369
- 5 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540
- 10 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982
 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200
 F-PLACE4000445
 F-PLACE4000450
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874
 F-PLACE4000487//Sialoporphin (gpl.115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075
- 15 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022
- 20 F-PLACE4000548
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:AF000986
 F-PLACE4000581
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080
- 25 F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:AB002446
- 30 F-PLACE4000650
 F-PLACE4000654
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688
- 35 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:AB014554
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877
- 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194
 F-THYRO1000034
 F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099
 F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326
- 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557
 F-THYRO1000085
 F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065
 F-THYRO1000107
- 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503
 F-THYRO1000121
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U07032
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:AF087142
- 55 F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203
 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

152936:D63475

F-THYRO1000186//H. sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs. 101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs. 101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs. 128818:AA976883

5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs. 43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs. 79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs. 104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs. 11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs. 160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs. 9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs. 60103:AB014590

F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs. 121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs. 25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C. elegans]//7.6e-92:431:99//Hs. 122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs. 80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs. 12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs. 7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs. 34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs. 118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs. 139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C. elegans]//5.8e-39:245:91//Hs. 119095:T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs. 156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs. 54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs. 115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs. 155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs. 2999:X52520

35 F-THYRO1000484//EST, Weakly similar to putative p150 [H. sapiens]//8.9e-22:248:76//Hs. 162011:AA513663

F-THYRO1000488

F-THYRO1000501//H. sapiens Staf50 mRNA//3.2e-75:615:77//Hs. 68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs. 119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs. 845:U31120

40 F-THYRO1000558//EST//1.3e-24:351:64//Hs. 142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs. 100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs. 112790:AA609949

45 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs. 151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs. 135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs. 162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs. 2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs. 89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs. 101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs. 32703:AA054125

F-THYRO1000658//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs. 116007:S79267

F-THYRO1000662

55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs. 105187:AI394157

F-THYRO1000676//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs. 116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H. sapiens]//0.46:368:57//Hs. 26557:AA480380

F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
 10 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
 F-THYRO1000787
 F-THYRO1000793
 F-THYRO1000796
 15 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:AB002446
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
 F-THYRO1000843
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.92381:AB007956
 25 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106489:AF042169
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
 F-THYRO1000983
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
 F-THYRO1001003
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
 F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z46788
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
 F-THYRO1001121//ESTs//0.92:257:61//Hs.18246:N95416
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
 F-THYRO1001173
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
 F-THYRO1001204
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

- F-THYRO1001320//ESTs//0.062:126.67//Hs.133296:AI311872
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560.68//Hs.153563:AF011333
 F-THYRO1001322//ESTs//0.12:238.61//Hs.29169:N66545
 F-THYRO1001347//ESTs//7.5e-61:293.99//Hs.129962:AA927207
 5 F-THYRO1001363//ESTs//1.0e-16:178.78//Hs.163954:N57939
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187.79//Hs.12385:AB007877
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740.97//Hs.138488:AB014607
 F-THYRO1001401//EST//4.6e-14:171.76//Hs.157587:AI356993
 10 F-THYRO1001403//ESTs//2.2e-50:464.79//Hs.118046:N49946
 F-THYRO1001405//ESTs//1.7e-44:226.99//Hs.156667:AI347694
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459.62//Hs.477:U05659
 F-THYRO1001411//ESTs//1.9e-41:342.78//Hs.146811:AA410788
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153.81//
 15 Hs.102877:U41315
 F-THYRO1001434//ESTs//1.1e-07:274.60//Hs.151093:AI224099
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653.71//Hs.44782:Z82215
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370.78//Hs.51048:X68830
 F-THYRO1001487//EST//1.0:88.71//Hs.160760:AI311943
 20 F-THYRO1001534//ESTs//1.2e-94:457.98//Hs.125523:AA883904
 F-THYRO1001537//ESTs//3.5e-94:469.97//Hs.106448:R76663
 F-THYRO1001541//EST//1.4e-10:158.65//Hs.145159:AI150211
 F-THYRO1001559//ESTs//1.4e-07:91.81//Hs.43507:N24046
 F-THYRO1001570//ESTs//2.3e-41:280.80//Hs.119752:AA703335
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546.95//Hs.25306:AF070572
 F-THYRO1001584//Human RCP3 mRNA, complete cds//0.14:335.58//Hs.82294:U27655
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165.84//Hs.75551:L12535
 F-THYRO1001602//ESTs//3.1e-42:350.80//Hs.138384:R72849
 F-THYRO1001605//EST//0.11:426.57//Hs.151206:AI126071
 30 F-THYRO1001617//ESTs//5.2e-43:345.81//Hs.8710:W07046
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108.86//Hs.141045:AA191659
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540.55//Hs.95958:M91463
 F-THYRO1001661//ESTs//0.12:53.92//Hs.151586:W45568
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780.98//
 Hs.118633:AJ225089
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212.73//Hs.78160:AF010238
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421.57//Hs.122908:AF070552
 F-THYRO1001706//ESTs//1.8e-24:142.95//Hs.112536:AI147691
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296.92//
 Hs.3826:U69560
 F-THYRO100173 8//EST//6.9e-30:180.94//Hs.58641:W81229
 F-THYRO1001745//ESTs//6.1e-49:244.98//Hs.97534:AA398813
 F-THYRO1001746//EST//0.96:119.63//Hs.144107:AI053590
 45 F-THYRO1001772//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:
 182.81//Hs.118053:N75725
 F-THYRO1001793//ESTs//1.9e-93:439.99//Hs.150116:AI299324
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168.67//Hs.11711:AB002295
 F-THYRO1001828
 50 F-THYRO1001854//EST//0.038:128.67//Hs.160649:AI241823
 F-THYRO1001895//Interleukin adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288.65//Hs.
 51061:M24283
 F-THYRO1001907//EST//1.9e-12:126.80//Hs.139296:AA350198
 F-VESEN1000122
 55 F-Y79AA1000013//ESTs//1.7e-72:369.96//Hs.97176:AA447885
 F-Y79AA1000033
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230.66//Hs.431:L13689
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629.64//Hs.75305:

U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706

F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080

F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R5969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs. Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310.94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150.64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174.66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385.58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772.60//Hs.82208:L46590
- 10 F-Y79AA1001061//ESTs//6.3e-41:303.84//Hs.55855:AA621381
- F-Y79AA1001068//EST//3.0e-23:165.90//Hs.157607:AI357511
- F-Y79AA1001077//ESTs//4.9e-40:237.94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247.66//Hs.55967:AF022654
- 15 F-Y79AA1001145//ESTs//1.3e-20:234.75//Hs.55855:AA621381
- F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155.63//Hs.5444:AB018293
- F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299.65//Hs.20191:U76248
- F-Y79AA1001185//ESTs//1.7e-56:318.93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs//9.1e-108:503.99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458.57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207.64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731.60//Hs.85279:U34879
- F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//4.0e-135:441.97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs//2.7e-21:157.88//Hs.163825:AI393240
- F-Y79AA1001299//Human In1 mRNA, complete cds//2.2e-116:323.93//Hs.155626:U04847
- F-Y79AA1001312//ESTs//3.7e-95:448.99//Hs.104469:W38395
- F-Y79AA1001323//ESTs//8.9e-50:340.86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505.70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424.96//Hs.154221:H23167
- F-Y79AA1001402//ESTs//1.0:245.62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311.61//Hs.83484:X07683
- F-Y79AA1001511//ESTs//9.9e-105:487.99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256.63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.96:202.61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs//2.6e-25:166.90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191.97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272.64//Hs.106070:U22398
- F-Y79AA1001585//ESTs//1.1e-84:473.93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs//1.7e-08:169.71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs//4.6e-07:429.59//Hs.160422:AI363426
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520.57//Hs.12334:AB014583
- 45 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421.94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386.60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243.61//Hs.3620:X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:428.59//Hs.162:X16302
- F-Y79AA1001696//ESTs//2.3e-44:249.94//Hs.163665:AA250877
- F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609.58//Hs.77297:L76191
- F-Y79AA1001711//ESTs//5.2e-29:224.83//Hs.100461:AI018620
- 55 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183.66//Hs.113082:AB007903
- F-Y79AA1001805//ESTs//1.1e-62:315.98//Hs.16141:W56079
- F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313.98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146.82//Hs.140588:H60533
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142.90//Hs.103349:AI141124
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215.67//Hs.104115:X52332
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412.62//Hs.106387:AF029778
 F-Y79AA1001875//ESTs//6.8e-09:198.67//Hs.138036:AI343173
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430.58//Hs.78501:L13720
 F-Y79AA1001963//ESTs//8.1e-131:642.97//Hs.54971:AI424382
 F-Y79AA1002027//ESTs//0.00042:58.91//Hs.5375:AA620611
 F-Y79AA1002083//ESTs//2.5e-51:285.95//Hs.117205:W88943
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348.88//Hs.18122:AI338045
 F-Y79AA1002093
 F-Y79AA1002103//ESTs//1.5e-15:223.71//Hs.97427:AA411865
 F-Y79AA1002115
 F-Y79AA1002125//ESTs//6.5e-41:206.99//Hs.159257:N40395
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165.90//Hs.6473:AA853955
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393.62//Hs.77864:AB014538
 F-Y79AA1002208//ESTs//2.7e-13:211.69//Hs.112469:AA598515
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldoteanax]//2.3e-113:568.96//Hs.111637:AA305890
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338.73//Hs.26662:U55984
 F-Y79AA1002211//ESTs//2.6e-15:121.75//Hs.159584:AA524477
 F-Y79AA1002220//EST//0.010:360.60//Hs.136341:AA482508
 F-Y79AA1002229//Homo sapiens mRNA for KIAA0086 gene, complete cds//0.0041:203.63//Hs.1560:D42045
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821.98//Hs.100729:AB014592
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525.59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748.98//Hs.96731:AB014555
 F-Y79AA1002298//ESTs//2.5e-05:115.77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622.97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126.94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587.58//Hs.2363:L36069
 F-Y79AA1002361//ESTs//8.7e-29:149.100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183.89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489.72//Hs.84112:X52142
 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94.71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263.69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313.80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249.61//Hs.162:X16302

Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,
 title of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005/ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME II [Caenorhabditis elegans]//5.6e-93.501.93/Hs.13015:AA628434

R-HEMBA1000030//Human POU domain protein (Bm-3b) mRNA, complete cds//0.83.314.61/Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282.89/Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528.72/Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155.63/Hs.149031:A1243340

R-HEMBA1000076//ESTs//3.1e-77:394.97/Hs.11742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228.85/Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502.90/Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514.94/Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435.77/Hs.153026:AB014540

R-nnnnnnnnnnnn/ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100/Hs.126925:AA931237

R-HEMBA1000158

R-nnnnnnnnnnnn/ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58.91/Hs.5570:AI377863

R-HEMBA1000180//ESTs//7.7e-90:461.95/Hs.159200:N50545

R-HEMBA1000185//ESTs//1.3e-72:37.196/Hs.134506:AA308366

R-HEMBA1000193//ESTs//4.2e-103:481.99/Hs.143251:AA769927

R-HEMBA1000201//Human Inl1 mRNA, complete cds//3.0e-25:137.99/Hs.155626:U04847

R-HEMBA1000213//ESTs//5.4e-85:465.94/Hs.23412:AA133311

R-HEMBA1000216//ESTs//3.0e-37:311.79/Hs.137875:AA993532

R-nnnnnnnnnnnn/EST//2.2e-100:498.96/Hs.161570:W80404

R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287.70/Hs.127649:AB007874

R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276.75/Hs.5737:AB007944

R-HEMBA1000244//ESTs//2.3e-88:455.96/Hs.8929:AA719019

R-HEMBA1000251//ESTs//0.96:411.56/Hs.120277:AI243808

R-HEMBA1000264//ESTs//3.7e-97:487.96/Hs.29258:W37424

R-nnnnnnnnnnnn/ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208.73/Hs.93332:AA811920

R-HEMBA1000282//ESTs//2.5e-38:216.94/Hs.120757:R92485

R-HEMBA1000288//ESTs//2.6e-43:289.96/Hs.151365:AA643962

R-HEMBA1000290//ESTs//5.1e-110:543.96/Hs.139068:AA516409

R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:102.677/Hs.129748:AB011099

R-nnnnnnnnnnnn/ESTs//7.4e-76:386.97/Hs.22276:AA191323

R-nnnnnnnnnnnn//Human Ca²⁺-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160.98/Hs.151301:U36448

R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489.99/Hs.108881:AI018024

R-nnnnnnnnnnnn/ESTs//9.3e-99:472.98/Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278.92/Hs.150815:AI302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270.88/Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531.96/Hs.61762:AI422243

R-HEMBA1000357//Human knpi repeat mna (cdna clone pod-kpni-4), 3' end//9.4e-89:432.87/Hs.139107:K00629

R-HEMBA1000366//ESTs//1.1e-99:524.95/Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355.96/Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388.77/Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337.83/Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428.62/Hs.2820:X64878

R-HEMBA1000392//ESTs//3.9e-105:531.96/Hs.130661:AI340248

R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447.75/Hs.42849:N31920

R-HEMBA1000411//ESTs, Weakly similar to ankryn 3, long form [H.sapiens]//6.1e-92:373.99/Hs.48675:AI005282

- R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
 R-HEMBA1000460
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155644:AF088219
 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277
 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
 R-nnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481
 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
 R-nnnnnnnnnnn
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
 R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.89519:L10717
 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
 R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
 R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736
 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

- R-HEMBA1000719//ESTs//8.4e-90:484.94//Hs.29005:AA477213
 R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572.95//Hs.28644:AI018612
 R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449.75//Hs.74478:U33931
 R-HEMBA1000727//ESTs//0.0047:267.60//Hs.133095:AA927777
 R-HEMBA1000747//EST//3.9e-20:160.85//Hs.99048:AA446110
 R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286.82//Hs.155644:AF088219
 R-HEMBA1000752//EST//0.041:39.94//Hs.127772:AA961131
 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309.75//Hs.10458:AF088219
 R-HEMBA1000773//EST//7.5e-05:201.63//Hs.122887:AA767612
 R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284.90//Hs.103458:X53795
 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291.87//Hs.154326:D42087
 R-HEMBA1000817//ESTs//8.3e-95:445.99//Hs.107357:AA983939
 R-HEMBA1000822//ESTs//1.1e-107:522.97//Hs.92832:AA631027
 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228.98//Hs.18192:AF048977
 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410.77//Hs.154103:AF061258
 R-HEMBA1000851
 R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284.80//Hs.159608:U46689
 R-HEMBA1000867//EST//2.0e-17:211.74//Hs.145670:AI265794
 R-HEMBA1000869//ESTs//3.1e-16:237.71//Hs.116518:AA653202
 R-HEMBA1000870//ESTs//1.6e-43:222.98//Hs.69564:AA203608
 R-HEMBA1000872//ESTs//1.9e-93:453.98//Hs.152622:AA594951
 R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329.79//Hs.155464:AF088219
 R-HEMBA1000908//ESTs//1.6e-51:291.92//Hs.12247:AI203154
 R-HEMBA1000910//EST//0.98:139.64//Hs.132687:AI033672
 R-HEMBA1000918//EST//9.6e-30:152.84//Hs.162136:AA526508
 R-HEMBA1000919
 R-HEMBA1000934//ESTs//4.1e-38:254.89//Hs.87784:AA460597
 R-HEMBA1000942//ESTs//3.5e-20:172.69//Hs.160065:AI018619
 R-HEMBA1000943//Homo sapiens mRNA for KIAA0743 protein, complete cds//1.3e-44:281.78//Hs.33187:AB018291
 R-HEMBA1000946//ESTs//1.6e-68:352.96//Hs.21331:H93074
 R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347.81//Hs.5247:AF029750
 R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362.84//Hs.159187:AB007977
 R-HEMBA1000971//ESTs//2.8e-41:246.91//Hs.104287:AI363498
 R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341.81//Hs.44766:AJ007590
 R-HEMBA1000974//ESTs//1.4e-32:166.100//Hs.149274:AI018170
 R-HEMBA1000975//Oxytocin receptor//2.7e-46:563.73//Hs.2620:X64878
 R-HEMBA1000985//ESTs//4.4e-05:125.69//Hs.147434:AI214464
 R-HEMBA1000986//ESTs//7.8e-44:266.84//Hs.163784:N54902
 R-HEMBA1000991//EST//1.4e-42:162.86//Hs.149580:AI281881
 R-HEMBA1001007
 R-HEMBA1001008//ESTs//2.3e-82:463.92//Hs.10339:AA058764
 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.126738:AA970836
 R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587.95//Hs.158287:AB007937
 R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140.95//Hs.58393:X05360
 R-HEMBA1001020//ESTs//0.52:86.72//Hs.69683:AA115292
 R-HEMBA1001022//ESTs//3.4e-18:102.100//Hs.63243:AI123912
 R-HEMBA1001024//ESTs//1.9e-07:262.61//Hs.124399:AA832336
 R-HEMBA1001026//ESTs//0.0017:142.67//Hs.144109:AI345543

- R-nnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616
 R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521
 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886
 5 R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
 R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420
 R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961
 R-HEMBA1001080
 10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA101788
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
 R-HEMBA1001094
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
 R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219
 15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
 20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219
 R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961
 25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194
 R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
 30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
 40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
 45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
 50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
 55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

- R-HEMBA1001413//ESTs//3.7e-66:321.98//Hs.152472:AA041199
R-HEMBA1001415
- R-HEMBA1001432//Putative mismatch repair/binding protein MSH3//7.9e-42:183.82//Hs.42674:U61981
R-HEMBA1001433//ESTs//1.4e-34:240.77//Hs.95611:U51704
- 5 R-HEMBA1001435//ESTs//5.6e-23:292.70//Hs.116315:AA629263
R-HEMBA1001442//ESTs//0.76:414.58//Hs.156189:AI419982
R-HEMBA1001446//ESTs//2.2e-95:447.99//Hs.154091:AA767546
R-HEMBA1001450//ESTs//1.0e-93:491.94//Hs.16130:AA195077
- 10 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304.88//Hs.23094:M19503
R-HEMBA1001455//ESTs//7.1e-103:482.99//Hs.97407:AI417220
R-HEMBA1001463
R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409.66//Hs.36232:D80008
R-HEMBA1001478
R-HEMBA1001497
- 15 R-HEMBA1001510//ESTs//3.3e-44:381.78//Hs.139882:AA864426
R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528.84//Hs.23094:M19503
R-HEMBA1001517//ESTs//5.8e-32:272.81//Hs.119512:AA487269
R-HEMBA1001522//ESTs//1.7e-84:364.95//Hs.117858:AA-702493
R-HEMBA1001526//ESTs//1.8e-93:527.93//Hs.10624:N64723
- 20 R-HEMBA1001533//ESTs//1.9e-42:211.100//Hs.55830:AA580270
R-HEMBA1001557//ESTs//4.2e-83:413.97//Hs.47546:AA181348
R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304.88//Hs.155464:AF088219
R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259.62//Hs.2229:X82324
R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456.77//Hs.159275:AF030880
- 25 R-HEMBA1001579//ESTs//0.11:299.60//Hs.106090:AA457030
R-HEMBA1001581//ESTs//0.016:350.61//Hs.124664:AI015552
R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251.63//Hs.146395:AB002329
R-HEMBA1001589
R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431.88//Hs.26625:W25874
- 30 R-HEMBA1001608//Human kpnI repeat mma (cdna clone pod-kpnI-8), 3' end//1.3e-73:533.82//Hs.103948:K00627
R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana] //4.5e-93:537.90//Hs.20218:AA628530
R-nnnnnnnnnnn/Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362.60//Hs.132206:AF039694
- 35 R-HEMBA1001636//ESTs//4.9e-53:267.97//Hs.47459:AA700158
R-HEMBA1001640//ESTs//2.9e-27:299.72//Hs.65236:AA927623
R-nnnnnnnnnnn/ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442.95//Hs.63888:AA203398
R-HEMBA1001655//ESTs//1.5e-101:516.95//Hs.86541:AA214554
R-HEMBA1001658
- 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427.61//Hs.106511:AF029343
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493.92//Hs.107254:AC005943
R-HEMBA1001675
- 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534.94//Hs.7381:AF038962
R-HEMBA1001681//ESTs//6.0e-49:292.92//Hs.65588:AA523424
R-HEMBA1001702//ESTs//9.0e-98:478.97//Hs.28661:AA805916
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483.96//Hs.31720:AB014598
- 50 R-HEMBA1001711//ESTs//5.8e-83:398.98//Hs.34804:AA514960
R-HEMBA1001712//ESTs//0.028:202.63//Hs.105790:AA528095
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236.98//Hs.132948:AA194452
- 55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166.88//Hs.155464:AF088219
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431.96//Hs.29203:AI344105
R-HEMBA1001731//EST//0.25:100.68//Hs.149171:AI245712

- R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353
R-HEMBA1001744
- R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162
- 5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243
- 10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823
R-nnnnnnnnnnn/Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334
- 15 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707
R-nnnnnnnnnnn/ESTs//2.2e-101:480:99//Hs.159940:AA971578
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210
- 20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517
- 25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein (alternative products)//1.9e-37:357:76//Hs.53217:Z48051
R-nnnnnnnnnnn/ESTs, Weakly similar to Trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R43329
- 30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438
- 35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145
- 40 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668
- 45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
- 50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
- 55 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

- R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
 R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369
 R-HEMBA1002113//Prostaglandin 12 (prostaglandin) synthase //1.4e-76:280:90//Hs.61333:D83402
 R-HEMBA1002119//Homo sapiens ORF12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
 R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674
 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
 R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
 R-HEMBA1002257
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822
 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
 R-nnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

[illegible]

R-HEMBA1002780/Homo sapiens DEC-205 mRNA, complete cds/4.2e-46:449.75/Hs.153563:AF013333

R-HEMBA1002794/ESTs/1.2e-11:55.97/Hs.19741:AI27909

R-HEMBA1002801/EST/1.0.00049:287.60/Hs.126466:AA913320

R-HEMBA1002810/Homo sapiens formin binding protein 21 mRNA, complete cds/1.4e-116:559.97/Hs.28307:AF071185

R-HEMBA1002816/Human plectin (PLEC1) mRNA, complete cds/0.28:281.62/Hs.79706:U53204

R-HEMBA1002826/EST/16.7e-25:134.99/Hs.134683:AI092013

R-HEMBA1002833/ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]/4.3e-25:137.98/Hs.5337:AA243757

R-HEMBA1002850/ESTs/0.010:323.57/Hs.18282:W67514

R-HEMBA1002863/ESTs/1.1e-67:359.94/Hs.124699:W27830

R-HEMBA1002876/ESTs/0.72:202.62/Hs.144816:AI220827

R-HEMBA1002886/EST/13.2e-85:401.99/Hs.96580:AA005670

R-HEMBA1002896/Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds/1.2e-107:541.95/Hs.33787:AF037261

R-HEMBA1002921/Human mRNA for KIAA0189 gene, complete cds/0.84:103.71/Hs.95140:D80011

R-HEMBA1002924/ESTs/3.5e-86:423.98/Hs.27513:N34820

R-HEMBA1002934/Human mRNA for KIAA0118 gene, partial cds/2.1e-50:308.88/Hs.154326:D42087

R-HEMBA1002935/ESTs/1.0e-73:384.95/Hs.118193:N74481

R-HEMBA1002937/ESTs/0.052:167.65/Hs.145504:AI254165

R-HEMBA1002939/ESTs/1.6e-94:467.97/Hs.9893:AA007679

R-HEMBA1002944/ESTs/2.7e-17:176.80/Hs.143768:AA229732

R-HEMBA1002951/ESTs/3.7e-119:565.98/Hs.16218:AI190892

R-HEMBA1002954/EST/0.076:285.58/Hs.98706:AA431085

R-HEMBA1002968/Thiopurine S-methyltransferase/1.9e-46:314.85/Hs.51124:AF019369

R-HEMBA1002970/EST/10.0.00050:164.64/Hs.129630:AA000405

R-HEMBA1002971/Homo sapiens mRNA for KIAA0679 protein, partial cds/2.3e-30:162.99/Hs.5734:AB014579

R-HEMBA1002973/Small inducible cytokine A5 (RANTES)/5.7e-42:318.81/Hs.155464:AF088219

R-nnnnnnnnnnn/ESTs/3.2e-18:102.100/Hs.146255:AA197064

R-HEMBA1002999/ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]/7.9e-113:560.96/Hs.125749:AJ377682

R-HEMBA1003021/Homo sapiens PYRIN (MEFV) mRNA, complete cds/3.3e-42:290.85/Hs.113283:AF108080

R-HEMBA1003033/ESTs/2.8e-77:417.94/Hs.138860:W47480

R-HEMBA1003034/ESTs/3.7e-42:429.74/Hs.132818:AI038577

R-HEMBA1003035/ESTs/0.025:156.64/Hs.8473:TA0827

R-HEMBA1003037/ESTs/0.69:381.57/Hs.47312:AI240386

R-HEMBA1003041/ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]/5.6e-34:280.79/Hs.114905:AA088442

R-HEMBA1003046/Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds/1.3e-119:578.97/Hs.44097:AF054182

R-HEMBA1003064/ESTs/7.8e-85:419.96/Hs.87020:AA0706627

R-HEMBA1003067/Von Hippel-Lindau syndrome/12.0e-30:299.75/Hs.78160:AF010238

R-HEMBA1003071/ESTs/2.3e-74:360.98/Hs.17270:AA071903

R-HEMBA1003077/ESTs, Weakly similar to KIAA0405 [H.sapiens]/1.1e-90:434.99/Hs.14146:W92235

R-HEMBA1003078/ESTs/5.9e-16:156.77/Hs.142684:AA902402

R-HEMBA1003079/ESTs/0.16:341.58/Hs.95923:AI075249

R-HEMBA1003083/Small inducible cytokine A5 (RANTES)/1.9e-39:284.83/Hs.155464:AF088219

R-HEMBA1003086/EST/1.0e-48:372.82/Hs.161917:AA483223

R-HEMBA1003098/ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]/4.2e-100:531.94/Hs.104800:AA709155

R-HEMBA1003098/ESTs/4.2e-107:537.96/Hs.107213:AA121624

R-HEMBA1003117/ESTs/2.4e-67:331.97/Hs.157158:AI150058

R-HEMBA1003129/Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds/2.1e-13:109.88/Hs.118717:U86751

R-HEMBA1003133/ESTs/1.1e-34:180.98/Hs.159387:AI370845

R-HEMBA1003136/ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]/9.2e-114:577.95/Hs.17059:AA088615

R-HEMBA1003142/Small inducible cytokine A5 (RANTES)/1.1e-45:285.88/Hs.155464:AF088219

- R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670
 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540
 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
 R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
 R-HEMBA1003215//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
 R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
 R-HEMBA1003281
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109
 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66e-64:76//Hs.117176:AF026029
 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204
 R-HEMBA1003417//ESTs//1.7e-24:188:85//Hs.70266:Z78309
 R-HEMBA1003418//ESTs//4.2e-74:396:94//Hs.55220:D11563
 R-HEMBA1003431//ESTs//3.1e-107:545:95//Hs.3494:AI421013
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351

- R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
 R-HEMBA1003568//ESTs//2.0e-10:148:98//Hs.118570:AI342058
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
- 5 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
- 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
 R-HEMBA1003615
- 15 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
 R-HEMBA1003637//ESTs, Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438
- 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
- 25 R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
- 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
 R-HEMBA1003692//Human cytochrome P450-11B (h11B3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
- 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064
 R-HEMBA1003714//VIAOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
- 40 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
- 45 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
- 50 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
- 55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

- R-HEMBA1003856//ESTs//8.2e-20:266.71//Hs.48312:N68161
 R-HEMBA1003864//ESTs//1.6e-99:528.93//Hs.26890:AA449033
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146.64//Hs.74648:M73547
 5 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295.98//Hs.161661:AA166911
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286.79//Hs.61408:AF070621
 R-HEMBA1003885//ESTs//4.6e-50:293.90//Hs.142314:AA347930
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294.86//Hs.13572:AF068179
 10 R-HEMBA1003902//ESTs//1.8e-43:300.85//Hs.146811:AA410788
 R-HEMBA1003908//ESTs//3.5e-91:477.94//Hs.6638:AA536187
 R-HEMBA1003926//ESTs//7.9e-44:294.87//Hs.164036:AA845659
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276.81//Hs.72660:AB011157
 R-HEMBA1003939
 15 R-HEMBA1003942//ESTs//1.6e-81:428.94//Hs.50418:AA524669
 R-HEMBA1003950//ESTs//8.1e-54:283.95//Hs.145528:AI261545
 R-HEMBA1003953//ESTs//3.8e-30:194.89//Hs.99681:AA504591
 R-HEMBA1003958//ESTs//4.0e-45:394.77//Hs.141602:N63562
 R-HEMBA1003959//ESTs//5.2e-28:197.86//Hs.9951:W56253
 R-HEMBA1003976//ESTs//2.0e-29:232.84//Hs.133947:AI074525
 20 R-HEMBA1003978//ESTs//3.2e-115:549.98//Hs.76798:AI050882
 R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:448.97//Hs.117834:AA766771
 R-HEMBA1003987//ESTs//8.1e-36:193.88//Hs.151844:N92756
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360.81//Hs.150275:D87682
 25 R-HEMBA1004000//EST//5.5e-62:308.97//Hs.50438:N74105
 R-HEMBA1004011//ESTs//8.6e-85:431.96//Hs.36185:R98989
 R-HEMBA1004012//ESTs//1.3e-40:309.83//Hs.140329:AA714011
 R-HEMBA1004015//ESTs//5.1e-97:453.99//Hs.111446:AI333774
 R-HEMBA1004024//ESTs//5.2e-19:159.79//Hs.138856:H47461
 30 R-HEMBA1004038//ESTs//1.3e-41:346.79//Hs.146173:AA906191
 R-HEMBA1004042//ESTs//0.0012:201.69//Hs.24248:AA528253
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H. sapiens]//1.5e-22:365.70//Hs.99692:AA811804
 R-HEMBA1004048//ESTs//9.5e-104:497.98//Hs.77735:AI125469
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176.96//Hs.8997:M11717
 35 R-HEMBA1004055//ESTs//1.7e-115:577.96//Hs.59503:W63754
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577.82//Hs.113283:AF018080
 R-HEMBA1004074//EST//1.0:152.61//Hs.149093:AI243988
 R-HEMBA1004086//ESTs//4.0e-53:266.98//Hs.34658:N98652
 R-HEMBA1004097//ESTs//4.4e-46:279.91//Hs.110533:H16251
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534.69//Hs.90998:D50918
 R-HEMBA1004132//ESTs//4.6e-47:316.96//Hs.141602:N63562
 R-HEMBA1004133
 R-HEMBA1004138//EST//1.7e-08:211.64//Hs.129189:AA988736
 R-HEMBA1004143//ESTs//4.0e-25:137.97//Hs.21307:AA203320
 45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191.86//Hs.155464:AF088219
 R-HEMBA1004150//GRANALCALCIN//0.99:357.59//Hs.79381:M81637
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313.84//Hs.154326:D42087
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563.96//Hs.59968:AF067855
 R-HEMBA1004199
 50 R-HEMBA1004200//EST//3.1e-89:441.97//Hs.141173:R97701
 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552.94//Hs.10092:AI189282
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275.98//Hs.15832:AB014518
 55 R-HEMBA1004207//Leptin receptor//1.1e-117:573.97//Hs.54515:U50748
 R-HEMBA1004225//EST//9.7e-34:186.95//Hs.137567:R20617
 R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117.91//Hs.92033:AA255832

- R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353
 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389
 R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258
 5 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284
 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962
 R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018
 10 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931
 R-nnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081
 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228
 15 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795
 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061
 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C. elegans]//3.6e-93:496:94//Hs.14337:AA534961
 20 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426
 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679
 R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281
 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714
 25 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240
 30 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353
 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494
 35 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155646:AF088219
 40 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
 45 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
 50 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
 R-HEMBA1004507
 R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
 55 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
 R-HEMBA1004554
 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

- R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]/1.0:305:60//Hs.30272:AA134913
 R-HEMBA1004577//ESTs/17.9e-50:319:89//Hs.22660:AA582243
 R-HEMBA1004586//ESTs/2.6e-73:384:96//Hs.9582:R39769
 R-nnnnnnnnnnnnn//ESTs/6.0e-22:190:82//Hs.42530:N41661
 5 R-HEMBA1004610//ESTs/1.2e-91:438:98//Hs.47823:AA780767
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501/4.6e-52:327:85//Hs.159897:AB007970
 R-HEMBA1004629//ESTs/2.3e-19:215:76//Hs.111995:AI375915
 R-HEMBA1004631//ESTs/3.6e-99:470:98//Hs.49303:AA810785
 10 R-HEMBA1004632//ESTs/1.0:128:66//Hs.159182:AA831152
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D.3.2 IN CHROMOSOME III [Caenorhabditis elegans]/4.8e-111:532:98//Hs.12263:AA282393
 R-HEMBA1004638//ESTs/1.2e-66:341:95//Hs.122687:AI278454
 R-HEMBA1004666//ESTs/2.1e-65:333:96//Hs.98873:AA625442
 15 R-HEMBA1004669//ESTs/0.00039:116:74//Hs.138725:N76348
 R-HEMBA1004670//ESTs/1.7e-16:116:89//Hs.56825:AI057560
 R-HEMBA1004672//EST/6.7e-76:315:97//Hs.20821:R19368
 R-HEMBA1004693//ESTs/6.4e-68:327:99//Hs.159066:AI093252
 R-HEMBA1004697//ESTs/9.3e-98:467:98//Hs.62637:AA043562
 20 R-HEMBA1004705//EST/0.0034:271:58//Hs.112503:AA599042
 R-HEMBA1004709//EST/1.3e-55:392:85//Hs.149580:AI281881
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)/1.9e-47:449:76//Hs.155464:AF088219
 R-HEMBA1004725//EST/1.8e-71:424:88//Hs.155712:AI309235
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer/2.1e-44:467:73//Hs.91916:AF035317
 25 R-HEMBA1004733//EST/0.99:84:65//Hs.161372:AI423151
 R-HEMBA1004734//ESTs/1.8e-82:421:96//Hs.21275:N73275
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)/9.5e-39:296:82//Hs.51187:U82828
 R-HEMBA1004748//ESTs/1.7e-43:166:86//Hs.37573:H59651
 30 R-HEMBA1004751//ESTs/8.0e-23:155:88//Hs.149464:AI279428
 R-HEMBA1004752//Thromboxane A2 receptor/2.7e-45:281:89//Hs.89887:D38081
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20/8.3e-67:475:84//Hs.8102:L06498
 R-HEMBA1004756//ESTs/2.0e-81:384:99//Hs.129545:N68679
 R-HEMBA1004758//EST/2.0e-43:367:80//Hs.133006:AI049504
 35 R-HEMBA1004763//ESTs/2.0e-108:567:94//Hs.3757:W87380
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]/1.4e-47:379:81//Hs.141273:H66705
 R-HEMBA1004770//ESTs/0.0014:246:61//Hs.124857:AA687092
 R-HEMBA1004771//ESTs/1.1e-12:323:63//Hs.124146:AA699633
 40 R-HEMBA1004776//ESTs/2.5e-112:567:95//Hs.12680:W74476
 R-HEMBA1004778//ESTs/1.4e-33:272:75//Hs.141123:AA848167
 R-nnnnnnnnnnnnn
 R-HEMBA1004803//ESTs/1.0e-48:319:86//Hs.139231:W87732
 R-HEMBA1004806
 45 R-HEMBA1004807//ESTs/6.2e-77:362:100//Hs.140945:N47676
 R-HEMBA1004816//EST/4.3e-18:246:72//Hs.150552:AI053784
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds/5.0e-14:141:85//Hs.80510:M74002
 R-HEMBA1004847
 50 R-HEMBA1004850//ESTs/1.2e-83:395:99//Hs.30925:AA577120
 R-HEMBA1004863//ESTs/7.5e-21:204:79//Hs.35036:H95267
 R-HEMBA1004864
 R-HEMBA1004865//EST/6.7e-18:191:75//Hs.129944:AA429362
 R-HEMBA1004880//EST/4.4e-70:346:98//Hs.145094:AA452409
 55 R-HEMBA1004889//ESTs/4.8e-117:496:97//Hs.15641:W63676
 R-HEMBA1004900//ESTs/1.2e-15:283:68//Hs.157606:AI357470
 R-HEMBA1004909//ESTs/7.3e-44:368:79//Hs.140329:AA714011
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds/4.6e-50:313:89//Hs.40100:AB002390

- R-HEMBA1004923//ESTs//0.013:162.64//Hs. 143655:AI128388
 R-HEMBA1004929//EST//2.3e-48:250.97//Hs. 131589:AI025053
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs. 1361:M55053
- 5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs. 18029:AI422883
 R-HEMBA1004934//ESTs//1.3e-103:522.96//Hs. 40415:AA037215
 R-HEMBA1004944//ESTs//6.0e-21:97.84//Hs. 141973:N21434
 R-HEMBA1004954//ESTs//7.9e-112:596.93//Hs. 6226:W61007
- 10 R-HEMBA1004956//ESTs//3.1e-58:280.100//Hs. 120750:AA741074
 R-HEMBA1004960//ESTs//6.9e-89:476.93//Hs. 163738:AA601040
 R-HEMBA1004972//ESTs//3.0e-72:381.95//Hs. 55014:AA934035
 R-HEMBA1004973//ESTs//2.7e-91:441.98//Hs. 28144:AI292065
 R-HEMBA1004977//ESTs//2.0e-95:446.99//Hs. 29690:AI168404
- 15 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187.67//Hs. 129734:AJ001683
 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305.91//Hs. 146395:AB002329
 R-HEMBA1004983//ESTs//0.16:482.57//Hs. 131929:AI021894
 R-HEMBA1004995
- 20 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482.78//Hs. 141601:N63520
 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551.96//Hs. 103180:AI365212
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542.94//Hs. 31921:AB014548
- 25 R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491.94//Hs. 16085:AI261382
 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312.85//Hs. 22271:D26067
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443.78//Hs. 139019:N95348
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542.87//Hs. 16258:AI376436
- 30 R-HEMBA1005050//ESTs//6.3e-46:311.86//Hs. 159510:AA297145
 R-HEMBA1005062//ESTs//1.1e-14:216.68//Hs. 129935:AA994451
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303.73//Hs. 79385:U90905
 R-HEMBA1005075//EST//0.65:214.62//Hs. 133991:AI075789
 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304.83//Hs. 85889:U17077
- 35 R-HEMBA1005083//ESTs//2.8e-74:356.98//Hs. 132272:AI393958
 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545.96//Hs. 11170:AF080561
 R-HEMBA1005113//ESTs//1.1e-101:512.95//Hs. 7972:AI052739
 R-HEMBA1005123//Ley L-L//3.6e-58:519.77//Hs. 37062:AC005952
- 40 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309.85//Hs. 19949:X98173
 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394.75//Hs. 67619:AB007957
 R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362.77//Hs. 132206:AF039694
- 45 R-HEMBA1005159//EST//7.4e-47:252.94//Hs. 134930:AI093397
 R-HEMBA1005185//ESTs//5.2e-48:305.89//Hs. 14920:AA910914
 R-HEMBA1005201//ESTs//4.7e-58:293.97//Hs. 23752:C05766
 R-HEMBA1005202//ESTs//1.0:169.59//Hs. 153423:AI198239
 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191.61//Hs. 26931:AF061836
- 50 R-HEMBA1005223//ESTs//0.75:90.70//Hs. 127446:AA167284
 R-HEMBA1005232//EST//0.056:162.67//Hs. 65649:F13687
 R-HEMBA1005241//ESTs//3.6e-113:564.96//Hs. 12770:W84331
 R-HEMBA1005244//ESTs//6.4e-22:118.100//Hs. 21396:AA114834
 R-HEMBA1005251//ESTs//8.5e-36:213.92//Hs. 161554:AA393896
- 55 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277.93//Hs. 72660:AB011157
 R-HEMBA1005274//ESTs//3.7e-65:322.98//Hs. 105166:AA668862
 R-HEMBA1005275//ESTs//2.1e-29:298.73//Hs. 33393:R83391
 R-HEMBA1005293//ESTs//3.5e-93:448.98//Hs. 12066:AI208611

- R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750
 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519
 R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046
 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169
 R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606
 R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144
 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350
 R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653
 R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:90//Hs.54486:X54150
 R-HEMBA1005394//ESTs, Weakly similar to coded for C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278
 R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725
 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059
 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391
 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961
 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353
 R-HEMBA1005472//Human kpnI repeat mma (cdna clone pcd-kpnI-8), 3' end//8.4e-73:464:87//Hs.103948:K00627
 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445
 R-HEMBA1005497
 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788
 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544
 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870
 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740
 R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322
 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045
 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350
 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S. cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103
 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
 R-HEMBA1005583//ESTs//3.3e-30:139:80//Hs.142273:W37905
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//ESTs/1.0e-12:313.64//Hs.162402:AA053125
R-HEMBA1005609//ESTs/0.49:278.58//Hs.76235:W65390
R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422
R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]/2.8e-95:539:92//Hs.19400:AA682845
R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor/1.5e-38:317.78//Hs.1721:X58377
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds/2.3e-11:279:65//Hs.15245:AF041081
R-HEMBA1005632//EST/1.5e-10:181.70//Hs.120259:AA731522
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234.80//Hs.10458:AF088219
R-HEMBA1005666//ESTs/2.3e-103:534.95//Hs.14512:AA205973
R-HEMBA1005670//ESTs/2.6e-39:166.81//Hs.139414:AI279477
R-HEMBA1005679//Esterase D/fornylglycine hydrolase/1.3e-50:322.88//Hs.82193:M13450
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343.81//Hs.154103:AF061258
R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds/0.0050:235.64//Hs.159437:U44060
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.7e-47:376.84//Hs.26988:U66406
R-HEMBA1005705//ESTs/3.0e-53:259.99//Hs.55314:AA772055
R-HEMBA1005717//EST//2.5e-59:287.99//Hs.146870:AI159943
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)/1.2e-45:398.79//Hs.155481:AJ006470
R-HEMBA1005737//ESTs/2.5e-57:416.83//Hs.23245:AA053815
R-nnnnnnnnnnnnn//EST/0.098:125.68//Hs.136945:AA765672
R-HEMBA1005755//EST//1.2e-22:180.84//Hs.141488:NA7096
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404.80//Hs.2217:U21936
R-HEMBA1005780//ESTs/1.3e-106:512.97//Hs.11901:AA173974
R-HEMBA10057813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195.84//Hs.10458:AF088219
R-HEMBA1005815//ESTs/7.6e-19:290.71//Hs.112218:AI038601
R-HEMBA1005822//ESTs/5.4e-49:246.98//Hs.34804:AA514960
R-HEMBA1005829//ESTs/2.7e-72:344.99//Hs.54548:AI039201
R-HEMBA1005834//ESTs/1.6e-44:317.82//Hs.157029:AI080618
R-HEMBA1005852//ESTs/1.6e-102:544.93//Hs.9911:AA098911
R-HEMBA1005853//EST/1.8e-78:398.95//Hs.140248:AA759717
R-HEMBA1005884//EST/2.6e-18:275.67//Hs.139357:AA420790
R-HEMBA1005891//ESTs/2.1e-89:427.98//Hs.67317:AI022252
R-HEMBA1005894
R-HEMBA1005909//ESTs/2.6e-91:436.99//Hs.147492:AI215686
R-HEMBA1005911//ESTs/1.1e-85:446.95//Hs.134494:AI076363
R-HEMBA1005921//ESTs/1.4e-84:428.95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446.75//Hs.59403:AB01098
R-HEMBA1005934//ESTs/0.20:142.65//Hs.97079:AA370867
R-HEMBA1005962//ESTs/1.8e-87:409.100//Hs.161292:AI199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580.95//Hs.26285:AF082516
R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45:551.70//Hs.148495:AF050199
R-HEMBA1005999//ESTs/7.5e-24:201.69//Hs.157029:AI080618
R-HEMBA1006002//ESTs/3.1e-112:573.95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0:105.63//Hs.145273:AI249436
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444.67//Hs.26450:AB018268
R-HEMBA1006035//ESTs/4.5e-94:465.97//Hs.44625:NA49951
R-HEMBA1006036//ESTs/6.1e-90:420.100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424.98//Hs.132551:AA948490
R-nnnnnnnnnnnnn

- R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
 R-HEMBA1006091//ESTs//2.0e-84:44:1:94//Hs.9658:AA506313
 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:326:82//
 5 Hs.73614:U83460
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
 10 R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:
 AB007958
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930
 15 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//
 20 Hs.23617:AA928683
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:
 AF083384
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.
 10552:AA524401
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:
 92//Hs.104129:AA923278
 R-nnnnnnnnnnn/H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
 30 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.
 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:
 U33931
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:
 AI204587
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:
 AB011166
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5:82:84//Hs.23094:M19503
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
 55 R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05;487.58//Hs.32963:D31784

R-HEMBA1006461//ESTs//5.1e-78;393.97//Hs.142677:R95895

R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17;342.63//Hs.111730:AA604403

R-HEMBA1006471//ESTs//3.8e-66;370.92//Hs.14063:T77441

R-HEMBA1006474

R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40;365.78//Hs.46468:U45984

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92;517.91//Hs.132243:Y07701

R-HEMBA1006486//EST//7.0e-47;240.76//Hs.161917:AA483223

R-HEMBA1006489//ESTs//2.1e-93;440.99//Hs.125264:AA873350

R-HEMBA1006492//ESTs//0.00034;52.90//Hs.163219:AA810720

R-HEMBA1006494//EST//1.8e-06;192.67//Hs.141401:H93387

R-HEMBA1006497//ESTs//6.2e-45;232.97//Hs.118015:N33317

R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16;135.72//Hs.2161:M62505

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117;570.96//Hs.153858:AB014566

R-HEMBA1006521//ESTs//9.9e-99;496.96//Hs.64906:AA677300

R-HEMBA1006530//ESTs//0.18;260.60//Hs.24970:A1057628

R-HEMBA1006535//GS1 PROTEIN//0.52;267.62//Hs.78991:M86934

R-HEMBA1006540//EST//0.016;43.66//Hs.148189:AA897331

R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48;287.91//Hs.79507:AB011154

R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109;547.96//Hs.21122:AA191594

R-HEMBA1006562//EST//1.1e-13;327.63//Hs.149641:AI283064

R-HEMBA1006566//ESTs//2.6e-59;311.97//Hs.146014:R51876

R-HEMBA1006569//ESTs//4.7e-89;458.96//Hs.42861:W47425

R-HEMBA1006579//ESTs//2.9e-19;110.99//Hs.126191:AA873876

R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29;276.76//Hs.144563:AF057280

R-HEMBA1006595//ESTs//1.3e-96;487.96//Hs.43228:N67390

R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44;291.85//Hs.155464:AF088219

R-HEMBA1006612

R-nnnnnnnnnnnn//ESTs//1.2e-25;225.80//Hs.138852:AA284247

R-HEMBA1006624//ESTs//1.9e-93;454.98//Hs.72531:AA773630

R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60;286.90//Hs.22271:D26067

R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91;426.100//Hs.139469:AI299889

R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37;186.100//Hs.109818.AA411185

R-HEMBA1006643//ESTs//1.8e-35;189.97//Hs.139640:AA846777

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108;567.94//Hs.6196:U40282

R-HEMBA1006652//ESTs//7.6e-100;536.93//Hs.142613:AA129427

R-HEMBA1006653//ESTs//2.0e-33;181.87//Hs.153599:AI282511

R-HEMBA1006665//EST//1.2e-13;141.72//Hs.145596:AI263102

R-HEMBA1006674//ESTs//3.1e-32;212.83//Hs.95115:AA206594

R-HEMBA1006678//ESTs//2.6e-95;510.93//Hs.39140:UA01842

R-HEMBA1006682//EST//1.4e-05;277.62//Hs.145762:AI269435

R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32;261.79//Hs.77579:AF013263

R-HEMBA1006696//ESTs//4.5e-95;448.99//Hs.155694:AI032695

R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92;483.94//Hs.6525:AI205313

R-HEMBA1006709//ESTs//3.4e-25;207.80//Hs.88617:AA872062

R-HEMBA1006717

R-HEMBA1006737//EST//5.9e-30;317.75//Hs.140568:AA826002

R-HEMBA1006744//Interleukin 10//3.7e-41;419.74//Hs.2180:M57627

R-HEMBA1006754//ESTs//1.2e-46;276.83//Hs.141254:IA334099

- R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:
 15 AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:
 AJ010841
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-
 40 40:163:83//Hs.152369:AA504818
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 R-HEMBA1007147
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
 R-nnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
 50 R-HEMBA1007178//ESTs//2.2e-57:368:90//Hs.21648:AI302954
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:
 55 AB018340
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

- R-HEMBA1007273//ESTs//1.0e-98:472.98//Hs.122610:AA807062
 R-HEMBA1007279//ESTs//3.3e-107:558.94//Hs.126480:AI221207
 R-HEMBA1007281//EST//0.074:244.63//Hs.29304:R73543
 R-HEMBA1007288//EST//9.4e-43:344.81//Hs.162112:AA524804
 5 R-HEMBA1007300//ESTs//0.096:371.57//Hs.102680:N52990
 R-HEMBA1007301
 R-HEMBA1007319//ESTs//7.7e-113:570.96//Hs.29263:AI337917
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311.64//Hs.142764:AA205569
 10 R-HEMBA1007322//Human kpni repeat mma (cdna clone pod-kpni-4), 3' end//5.7e-49:383.83//Hs.139107:K00629
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371.79//Hs.154069:U06452
 R-HEMBA1007341//EST//3.0e-17:291.68//Hs.150788:AI301848
 15 R-HEMBA1007342//EST//2.7e-11:263.67//Hs.145259:AI218684
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368.82//Hs.153563:AF011333
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341.71//Hs.111730:AA604403
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292.83//Hs.129708:AF064090
 20 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311.87//Hs.66710:X96969
 R-HEMBA1000024//ESTs//7.5e-21:234.76//Hs.157049:AI345418
 R-HEMBA1000025//ESTs//2.2e-36:371.78//Hs.56562:AA056332
 R-HEMBA1000030//ESTs//3.2e-76:373.97//Hs.140190:AA701449
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME
 25 III [Caenorhabditis elegans]//6.0e-92:477.95//Hs.4877:AA418465
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467.97//Hs.20815:AF084928
 R-HEMBA1000039//ESTs//1.8e-43:361.71//Hs.108206:N64702
 R-HEMBA1000044//EST//7.6e-70:367.95//Hs.140860:R42954
 30 R-HEMBA1000048//EST//1.5e-45:262.91//Hs.157627:AI357802
 R-HEMBA1000050//ESTs//0.039:91.74//Hs.163189:AA236903
 R-HEMBA1000054//ESTs//3.0e-104:550.94//Hs.152395:AA533107
 R-HEMBA1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350.99//Hs.116490:AA659584
 35 R-HEMBA1000059//ESTs//1.7e-10:200.70//Hs.163954:N57939
 R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337.80//Hs.4953:D63997
 R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487.70//Hs.153014:AB002353
 R-HEMBA1000099//ESTs//5.7e-37:353.75//Hs.22910:W18193
 R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:296.69//Hs.153026:AB014540
 40 R-HEMBA1000113//EST//8.2e-94:437.100//Hs.136893:AA805239
 R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428.95//Hs.6315:Y15521
 R-HEMBA1000136//ESTs//0.043:262.59//Hs.61304:AA025692
 R-HEMBA1000141//ESTs//5.0e-38:254.79//Hs.141658:N77915
 45 R-HEMBA1000144//ESTs//9.6e-05:235.60//Hs.61700:AA033951
 R-HEMBA1000173//EST//9.6e-44:258.76//Hs.161917:AA483223
 R-HEMBA1000175//ESTs//4.8e-98:475.97//Hs.149740:AI199558
 R-HEMBA1000198//ESTs//1.0:123.62//Hs.116602:AA665965
 R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302.86//Hs.153014:AB002353
 50 R-HEMBA1000217//ESTs//2.2e-105:496.99//Hs.65973:AI339364
 R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292.79//Hs.133089:AF064019
 R-HEMBA1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449.89//Hs.16803:AA843214
 55 R-HEMBA1000240//ESTs//1.1e-109:536.97//Hs.13528:AA523106
 R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323.83//Hs.155464:AF088219
 R-HEMBA1000250//EST//8.8e-12:284.64//Hs.145960:AI276783
 R-HEMBA1000258//EST//4.5e-14:315.66//Hs.162651:AA584782

- R-HEMBB1000264
R-HEMBB1000266/ESTs, Weakly similar to similar to the beta transducin family [C.elegans]/2.7e-102:556:93//
Hs.16079:AA083522
- 5 R-HEMBB1000272/ESTs/4.3e-91:480:94//Hs.107467:H11385
R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:
AB011129
R-HEMBB1000284/ESTs/4.8e-64:389:91//Hs.118043:N50458
R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353
- 10 R-HEMBB1000312/ESTs/6.0e-23:272:73//Hs.121354:AA758601
R-HEMBB1000317/ESTs/7.5e-90:424:99//Hs.150042:A1298034
R-HEMBB1000318//Small inducible cytokine A5 (RANTES)/3.3e-41:318:80//Hs.155464:AF088219
R-HEMBB1000335/ESTs/3.7e-15:324:65//Hs.85077:AA968576
R-HEMBB1000336/ESTs/6.4e-76:402:95//Hs.17207:H92480
R-HEMBB-1000337/ESTs/2.1e-80:391:97//Hs.118990:A1378084
- 15 R-HEMBB1000338//Small inducible cytokine A5 (RANTES)/4.0e-39:274:85//Hs.155464:AF088219
R-HEMBB1000339/EST/5.8e-41:336:79//Hs.151873:AA205736
R-HEMBB1000341/ESTs/3.8e-19:310:68//Hs.37573:H59651
R-HEMBB1000343/EST/1.1e-77:396:95//Hs.162664:AA605020
R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008
- 20 R-HEMBB1000369/ESTs/1.6e-21:234:73//Hs.111583:AA463590
R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487/2.3e-56:335:77//Hs.
92381:AB007956
R-HEMBB1000376//H. sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969
R-HEMBB1000391/ESTs/6.6e-50:316:88//Hs.142259:AA828840
- 25 R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642
R-HEMBB1000402//H. sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
R-HEMBB1000404/EST/0.088:298:59//Hs.61607:AA032026
R-HEMBB1000420/EST/2.2e-78:376:98//Hs.160787:A1336591
R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
- 30 R-HEMBB1000438/ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/0.30:214:63//
Hs.142209:AA873303
R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
R-HEMBB1000449/ESTs/7.8e-59:332:92//Hs.87013:AA130221
R-HEMBB1000455/EST/4.8e-14:421:65//Hs.68832:AA086438
- 35 R-HEMBB1000472/ESTs/1.1e-104:505:98//Hs.132824:A1033396
R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
R-HEMBB1000487/EST//0.78:67:68//Hs.134601:A1081506
R-HEMBB1000490//Small inducible cytokine A5 (RANTES)/4.0e-39:320:80//Hs.155464:AF088219
R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
- 40 R-HEMBB1000493/ESTs/7.1e-18:150:82//Hs.142068:AA176125
R-HEMBB1000510/EST//1.4e-45:139:97//Hs.152260:AA489703
R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
R-HEMBB1000530/ESTs/2.7e-73:425:90//Hs.141254:A1334099
- 45 R-HEMBB1000550/EST/2.9e-111:113:79//Hs.161503:N68662
R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:932:81//Hs.97206:
AF052288
R-HEMBB1000556/ESTs/1.1e-94:529:92//Hs.33476:N36986
R-HEMBB1000564/ESTs/1.3e-19:128:91//Hs.142058:N34258
- 50 R-HEMBB1000573/ESTs/1.6e-86:494:90//Hs.120979:A1160709
R-HEMBB1000575/ESTs/1.6e-45:232:74//Hs.141019:AA267618
R-HEMBB1000586/ESTs/5.1e-42:281:83//Hs.138852:AA284247
R-HEMBB1000589/ESTs/1.0e-10:184:71//Hs.142677:R95895
R-HEMBB1000591/ESTs/3.2e-40:406:75//Hs.138787:H73704
- 55 R-HEMBB1000592/ESTs/1.8e-97:455:99//Hs.94229:W65391
R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
R-HEMBB1000623/ESTs/8.3e-47:277:92//Hs.6045:W67125
R-HEMBB1000630/ESTs/5.1e-106:538:96//Hs.13422:A1082249

- R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
 R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
 R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554.D38522
 R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
 R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
 R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100
 R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
 R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.14107:W94988
 R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
 R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
 R-nnnnnnnnnnn/Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
 R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H. sapiens]//3.9e-50:245:99//Hs.111730:AA604403
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
 R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:A1281881
 R-HEMBB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:A1125541
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73734:Z23091
 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
 R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
 R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:A1281881
 R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
 R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
 R-HEMBB1000840//ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
 R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
 R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.51048:X68830
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:A1281881
 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
 R-HEMBB1000947//ESTs, Weakly similar to F2E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503
 R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
 R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
 R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
 R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

- R-HEMBB1001004//ESTs//5.7e-70:362.95//Hs.6434:W27112
 R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]/2.3e-25:339.71//Hs.129992:H58762
- 5 R-HEMBB1001011//ESTs//4.0e-53:325.92//Hs.33268:A191214
 R-HEMBB1001014//ESTs//1.3e-46:323.83//Hs.163980:AA715814
 R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305.76//Hs.113283:AF018080
 R-HEMBB1001024//ESTs//8.5e-47:374.80//Hs.141602:N63562
 R-HEMBB1001037//ESTs//2.6e-47:282.91//Hs.155384:Z78385
 R-HEMBB1001047//EST//6.2e-33:232.74//Hs.160146:AI049975
- 10 R-HEMBB1001051//ESTs//7.9e-39:385.98//Hs.95290:AA046107
 R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497.91//Hs.15832:AB014518
 R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125.81//Hs.5737:AB007944
- 15 R-HEMBB1001060//ESTs//1.9e-37:541.69//Hs.141534:N64785
 R-HEMBB1001063//ESTs//4.7e-42:269.88//Hs.55855:AA621381
 R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512.97//Hs.12953:AF034803
 R-HEMBB1001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233.70//Hs.37181:D64108
 R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299.82//Hs.153014:AB002353
- 20 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296.87//Hs.113283:AF018080
 R-HEMBB1001114//ESTs//6.2e-44:293.86//Hs.70279:AA757426
 R-HEMBB1001117//ESTs//1.1e-80:471.90//Hs.61935:T75092
 R-HEMBB1001119//ESTs//4.0e-38:213.84//Hs.109140:AI289942
 R-HEMBB1001126
- 25 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285.73//Hs.554:M25077
 R-HEMBB1001137//ESTs//4.6e-10:66.100//Hs.74924:AI332962
 R-HEMBB1001142//EST//6.4e-48:315.85//Hs.149580:AI281881
 R-HEMBB1001151
- 30 R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.3e-65:331.96//Hs.154179:AA579197
 R-HEMBB1001169//Oxytocin receptor//1.5e-25:165.73//Hs.2820:X64878
 R-nnnnnnnnnnnnn//ESTs//3.5e-41:233.93//Hs.129218:AA991162
 R-HEMBB1001177
- 35 R-HEMBB1001182//ESTs//1.9e-86:455.95//Hs.6937:AA524349
 R-HEMBB1001199
 R-HEMBB1001208//ESTs//3.3e-43:216.99//Hs.121806:N71183
 R-HEMBB1001209//ESTs//6.7e-80:409.96//Hs.141185:R99549
 R-HEMBB1001210//ESTs//2.2e-46:290.88//Hs.103329:D11573
- 40 R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody I4A))/3.1e-44:298.87//Hs.103458:X53795
 R-HEMBB1001221//ESTs//9.4e-75:353.100//Hs.151504:AA550817
 R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]/3.8e-80:400.96//Hs.71873:AA148213
- 45 R-HEMBB1001242//ESTs//1.6e-63:404.87//Hs.25534:AA149560
 R-HEMBB1001249//ESTs//3.8e-34:360.70//Hs.150727:AI292236
 R-HEMBB1001253//EST//0.0011:84.77//Hs.124579:AA853987
 R-HEMBB1001254//ESTs//4.5e-95:444.99//Hs.161059:AI431268
 R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524.73//Hs.159897:AB007970
- 50 R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323.84//Hs.154326:D42087
 R-HEMBB1001282//EST//2.9e-78:401.96//Hs.72871:AA169412
 R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]/2.6e-104:515.97//Hs.16606:W81021
- 55 R-HEMBB1001289//ESTs//7.8e-45:440.75//Hs.44702:AI148840
 R-HEMBB1001294//ESTs//1.9e-100:476.99//Hs.109017:AI057112
 R-HEMBB1001302
 R-HEMBB1001304//ESTs//4.0e-92:431.99//Hs.113750:AI091154

R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627
 R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627
 R-HEMBB1001317//Human cytochrome P450-11B (h11B3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873
 5 R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754
 R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
 R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
 R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
 R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470
 10 R-HEMBB1001346
 R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
 R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
 R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055
 15 R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087
 R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617
 R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155644:AF088219
 R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
 R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699
 20 R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
 R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
 R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342
 R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
 R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
 25 R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
 R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
 R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
 R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
 R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
 30 R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
 R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
 R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468
 R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
 R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515
 35 R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280
 R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
 R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
 40 R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
 R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
 R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.6158:AB007869
 R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
 R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
 45 R-HEMBB1001564//EST//1.7e-35:141:81//Hs.162197:AA53521
 R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
 R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
 R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
 R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
 50 R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
 R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
 R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
 R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
 R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
 55 R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
 R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
 R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

- R-HEMBB1001668//ESTs//0.73:212.62//Hs.8928:N32572
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573.97//Hs.24439:AB014546
- 5 R-HEMBB1001684//ESTs, Moderately similar to Tbcd [M.musculus]//5.4e-106:523.97//Hs.26939:AA804534
 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292.86//Hs.96337:AA225358
 R-HEMBB1001695//ESTs//3.7e-101:539.94//Hs.78289:R60867
 R-HEMBB1001704//EST//0.96:248.57//Hs.163025:AA703038
 R-HEMBB1001706//ESTs//1.3e-39:308.81//Hs.141318:N171080
- 10 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277.73//Hs.142764:AA205569
 R-HEMBB1001717//ESTs//1.6e-34:225.87//Hs.57883:AA218645
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158.71//Hs.141263:H64113
- 15 R-HEMBB1001736//ESTs//0.0035:223.60//Hs.21354:AA203403
 R-HEMBB1001747//EST//9.9e-55:293.81//Hs.112866:AA620488
 R-HEMBB1001749//ESTs//2.5e-13:95.91//Hs.139888:N25287
 R-HEMBB1001753//ESTs//2.6e-07:141.70//Hs.144604:AI052059
 R-HEMBB1001756//EST//2.6e-06:165.64//Hs.121195:AA757211
- 20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264.74//Hs.70008:L00352
 R-HEMBB1001762//ESTs//2.1e-81:447.93//Hs.152766:AA211369
 R-HEMBB1001785//ESTs//0.040:390.58//Hs.116651:AA993406
 R-HEMBB1001797//ESTs//2.1e-90:428.99//Hs.8958:AA169253
- 25 R-HEMBB1001802//Desmin//9.9e-95:497.93//Hs.119104:M63391
 R-HEMBB1001812//ESTs//1.2e-12:91.78//Hs.138852:AA284247
 R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143.76//Hs.23094:M19503
 R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (CPIP1) mRNA, complete cds//5.5e-106:498.98//Hs.159396:AF056209
- 30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288.73//Hs.67619:AB007957
 R-HEMBB1001839
 R-HEMBB1001850//EST//0.020:119.68//Hs.32767:H38125
 R-HEMBB1001863//ESTs//4.5e-17:226.72//Hs.157253:AI357539
- 35 R-HEMBB1001867//ESTs//2.3e-16:254.68//Hs.123664:AA806106
 R-HEMBB1001868//EST//9.8e-30:155.100//Hs.160572:AA888397
 R-HEMBB1001869//ESTs//2.8e-42:376.78//Hs.141973:N21434
 R-HEMBB1001872//EST//0.85:156.64//Hs.119501:AA487980
 R-HEMBB1001874//EST//0.64:107.70//Hs.147482:AI215572
- 40 R-HEMBB1001875//EST//0.079:199.59//Hs.121810:AA775240
 R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297.88//Hs.89887:D38081
 R-HEMBB1001899//ESTs//6.3e-68:323.100//Hs.121538:AA609310
 R-HEMBB1001905//ESTs//4.4e-19:227.73//Hs.146173:AA906191
 R-HEMBB1001906//ESTs//1.6e-90:463.95//Hs.28266:H46725
- 45 R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557.64//Hs.26929:AF008915
 R-HEMBB1001910//EST//6.0e-37:308.78//Hs.162197:AA535216
 R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367.79//Hs.5247:AF029750
 R-HEMBB1001915//ESTs//3.1e-73:395.93//Hs.17054:AI139897
 R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323.88//Hs.40100:AB002390
- 50 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRP129//7.4e-38:531.70//Hs.153086:Y11251
 R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199.77//Hs.149323:AB002325
 R-HEMBB1001930//EST//1.9e-18:136.78//Hs.132635:AI032875
 R-HEMBB1001944//EST//0.034:228.57//Hs.93664:N23366
- 55 R-HEMBB1001945//ESTs//1.8e-83:439.95//Hs.7341:N57875
 R-HEMBB1001947//ESTs//5.6e-109:533.97//Hs.48855:AA134589
 R-HEMBB1001950//ESTs//1.5e-107:583.93//Hs.8033:N94998
 R-HEMBB1001952//ESTs//3.1e-40:283.85//Hs.146811:AA410788

- R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284.83//Hs.74554:D38522
 R-HEM BB1001957//EST//4.8e-50:382.81//Hs.149580:AI281881
 R-HEM BB1001962//ESTs//1.5e-20:143.88//Hs.11924:W26972
 R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296.88//Hs.153468:AB011147
 R-HEM BB1001973//ESTs//1.4e-48:303.88//Hs.132722:AA618531
 R-HEM BB1001983//ESTs//2.6e-72:374.95//Hs.141022:H06475
 R-HEM BB1001988//ESTs//2.0e-31:204.88//Hs.142531:N91572
 R-HEM BB1001990//ESTs//9.4e-115:574.96//Hs.44426:AA173223
 R-HEM BB1001996
 R-HEM BB1001997//ESTs//7.6e-78:380.98//Hs.32682:H37798
 R-HEM BB1002002//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//3.0e-18:222.71//Hs.103948:K00627
 R-HEM BB1002005//EST//2.2e-41:339.80//Hs.160833:AI345334
 R-HEM BB1002009//EST//2.9e-44:245.94//Hs.28788:R66896
 R-HEM BB1002015//EST//0.0027:198.63//Hs.160868:AI359052
 R-HEM BB1002042//ESTs//1.1e-75:529.84//Hs.106919:AA523900
 R-HEM BB1002043//ESTs//7.9e-40:292.83//Hs.70279:AA757426
 R-HEM BB1002044//ESTs//2.1e-92:460.94//Hs.115897:AA156638
 R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301.85//Hs.113283:AF018080
 R-HEM BB1002049//ESTs//3.8e-77:409.94//Hs.122624:R82638
 R-HEM BB1002050//ESTs//8.7e-45:330.82//Hs.44702:AI148840
 R-HEM BB1002068//ESTs//8.3e-70:333.99//Hs.134807:AI090671
 R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486.81//Hs.129735:AF010144
 R-HEM BB1002092//ESTs//6.5e-46:331.83//Hs.22910:W18193
 R-HEM BB1002094//EST//3.6e-45:280.88//Hs.149580:AI281881
 R-HEM BB1002115
 R-HEM BB1002139//ESTs//4.2e-45:318.85//Hs.107657:AA126814
 R-HEM BB1002142//Homo sapiens haemopoietic progenitor/homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281.88//Hs.125231:AF068006
 R-HEM BB1002152//EST//4.3e-39:250.89//Hs.156552:AA833553
 R-HEM BB1002189//H. sapiens mRNA for translin associated protein X//1.4e-47:328.85//Hs.96247:X95073
 R-HEM BB1002190//ESTs//8.3e-05:122.70//Hs.41974:AF039185
 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398.69//Hs.301:U18934
 R-HEM BB1002217//EST//6.6e-50:303.89//Hs.149580:AI281881
 R-HEM BB1002218//ESTs//2.3e-19:150.96//Hs.136031:W95841
 R-HEM BB1002232//ESTs//8.9e-47:445.77//Hs.163971:N27584
 R-HEM BB1002247//EST//6.6e-09:236.65//Hs.130578:AI004631
 R-HEM BB1002249//ESTs//5.2e-16:325.64//Hs.156253:AI334807
 R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590.88//Hs.23094:M19503
 R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342.83//Hs.84123:AB002363
 R-HEM BB1002266//ESTs//4.4e-98:472.98//Hs.65366:AI189112
 R-HEM BB1002280//EST//2.9e-41:247.90//Hs.161917:AA483223
 R-HEM BB1002300//ESTs//8.4e-19:229.75//Hs.138463:N72305
 R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138.67//Hs.155174:AB007892
 R-HEM BB1002327//EST//0.042:249.61//Hs.121097:AA714637
 R-HEM BB1002329//ESTs//1.7e-94:453.99//Hs.7114:R24312
 R-HEM BB1002340//ESTs//5.8e-15:163.77//Hs.26378:H10228
 R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85e-46:84//Hs.42644:AJ010841
 R-HEM BB1002358//ESTs//2.0e-52:319.81//Hs.140255:AA078322
 R-HEM BB1002359//ESTs//2.7e-106:517.97//Hs.13634:AI051613
 R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360.65//Hs.74554:D38522
 R-HEM BB1002371//Catalase//3.2e-22:235.77//Hs.76359:X04085
 R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120.78//Hs.142296:AF072467
 R-HEM BB1002383//ESTs//3.5e-108:520.98//Hs.45140:D80055
 R-HEM BB1002387
 R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

- 168:77//Hs.133526:N21103
R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/3.2e-57:304:90//Hs.144563:AF057280
- 5 R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353
R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087
R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.16240:AA460083
R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
- 10 R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142
R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278
- 15 R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
R-HEMBB1002522//Human putative transmembrane receptor IL-1R α mRNA, complete cds//0.50:142:69//Hs.159301:U43672
R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605
R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
- 20 R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.51048:X68830
R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
- 25 R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087
R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
- 30 R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
R-HEMBB1002610//ESTs, Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977
- 35 R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917
R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
- 40 R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219
R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881
R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775
R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339
- 45 R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646
R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753
R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099
R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398
- 50 R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547
R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
- 55 R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219
R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

- R-MAMMA1000045//ESTs//1.0e-38:225.92//Hs.142567:AA287165
 R-MAMMA1000055//EST//0.14:91.67//Hs.144061:AA996350
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545.83//Hs.69747:M35531
- 5 R-MAMMA1000069//ESTs//8.0e-108:546.96//Hs.44856:N37065
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313.83//Hs.46918:AF052099
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546.94//Hs.7779:AA045241
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287.71//Hs.136063:U51713
- 10 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334.86//Hs.70008:L00352
 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96.80//Hs.115088:AA230172
- 15 R-MAMMA1000129//EST//2.8e-64:310.99//Hs.136394:AA523577
 R-MAMMA1000133
 R-MAMMA1000134//ESTs//1.1e-21:152.87//Hs.163747:AA174017
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288.78//Hs.159897:AB007970
- 20 R-MAMMA1000143//EST//5.0e-52:314.89//Hs.149580:AI281881
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562.75//Hs.77579:AF013263
 R-MAMMA1000163//ESTs//2.8e-92:457.96//Hs.114413:AA884787
 R-MAMMA1000171//Homo sapiens mRNA for putative lipolic acid synthetase, partial//2.5e-39:173.83//Hs.53531:AJ224162
- 25 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63.90//Hs.90367:AI357069
 R-MAMMA1000175//EST//0.66:217.58//Hs.146444:AI127611
 R-MAMMA1000183//ESTs//6.7e-30:341.73//Hs.125254:AA872054
- 30 R-MAMMA1000198//EST//2.8e-45:185.88//Hs.149580:AI281881
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272.90//Hs.68398:AA421103
 R-MAMMA1000227//EST//2.4e-39:388.76//Hs.144175:H70425
 R-MAMMA1000241//EST//0.0027:263.61//Hs.37532:H57946
- 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322.86//Hs.15519:AB018315
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315.83//Hs.129708:AF064090
 R-MAMMA1000257//EST//1.6e-62:330.93//Hs.141728:W73041
- 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141.81//Hs.78160:AF010238
 R-MAMMA1000266//ESTs//3.4e-34:150.81//Hs.163980:AA715814
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304.78//Hs.159187:AB007977
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380.71//Hs.51124:AF019369
- 45 R-MAMMA1000278//ESTs//5.2e-99:504.95//Hs.8494:W72694
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295.83//Hs.92381:AB007956
 R-MAMMA1000284//EST//4.1e-10:151.73//Hs.60742:AA017066
 R-MAMMA1000287
- 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50.84//Hs.155174:AB007892
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468.76//Hs.22271:D26067
 R-MAMMA1000309//ESTs//1.7e-94:491.94//Hs.135106:AI335251
 R-MAMMA1000312//ESTs//8.9e-74:377.96//Hs.133163:AI051434
 R-MAMMA1000313//EST//8.3e-19:294.62//Hs.127400:AA954491
- 55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278.97//Hs.139170:AA662988
 R-MAMMA1000339//EST//6.8e-44:169.89//Hs.149580:AI281881
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204.61//Hs.154919:AB014525

- R-MAMMA1000348//ESTs//3.3e-34:320.75//Hs.139158:AA226159
 R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172.61//Hs.11463:AA535912
- 5 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212.82//Hs.154326:D42087
 R-MAMMA1000361//ESTs//3.1e-17:188.68//Hs.164036:AA845659
 R-MAMMA1000372//ESTs//1.0e-46:307.85//Hs.145032:AA343523
 R-MAMMA1000385//ESTs//8.2e-97:467.98//Hs.152282:AA412065
 R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
- 10 R-MAMMA1000395//ESTs//1.9e-57:292.96//Hs.11365:AB01060
 R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316.81//Hs.138698:N38973
 R-MAMMA1000410//Archaea//1.8e-40:443.74//Hs.33642:X81198
 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304.72//Hs.119387:AB007958
- 15 R-MAMMA1000414//ESTs//2.9e-27:181.87//Hs.141254:AI334099
 R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282.82//Hs.97203:U83171
 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372.80//Hs.89887:D38081
- 20 R-MAMMA1000422//ESTs//0.077:240.62//Hs.123136:AA631067
 R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375.81//Hs.40100:AB002390
 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418.75//Hs.154069:U06452
 R-MAMMA1000429//ESTs//3.9e-113:565.96//Hs.5076:N53461
- 25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302.85//Hs.97203:U83171
 R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344.81//Hs.13572:AF068179
 R-MAMMA1000446//ESTs//1.0:236.60//Hs.126958:AI147447
 R-MAMMA1000458
- 30 R-MAMMA1000468//ESTs//4.4e-51:271.96//Hs.6839:AA055176
 R-MAMMA1000472//ESTs//5.4e-39:146.86//Hs.141581:AA315361
 R-MAMMA1000478//ESTs//2.3e-74:365.98//Hs.140591:AA828959
 R-MAMMA1000483//ESTs//9.9e-23:235.75//Hs.163592:AA280886
 R-MAMMA1000490//EST//2.1e-80:500.87//Hs.142137:AA213759
- 35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)/4.7e-43:283.86//Hs.155464:AF088219
 R-MAMMA1000501//ESTs//4.2e-37:250.86//Hs.141323:N80390
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459.75//Hs.40100:AB002390
 R-MAMMA1000522//ESTs//9.5e-16:226.70//Hs.116673:AA669267
 R-MAMMA1000559//ESTs//5.2e-34:244.84//Hs.150727:AI292236
- 40 R-MAMMA1000565//EST//2.7e-38:386.76//Hs.162404:AA573131
 R-MAMMA1000567//EST//0.33:49.79//Hs.147754:AI220561
 R-MAMMA1000576//ESTs//4.9e-57:348.89//Hs.108921:N31211
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373.77//Hs.6200:AB007872
 R-MAMMA1000585//ESTs//5.1e-40:337.78//Hs.130815:AA936548
- 45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)/3.0e-45:225.80//Hs.155464:AF088219
 R-MAMMA1000597//ESTs//2.0e-98:461.99//Hs.43212:AA993042
 R-MAMMA1000605//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500.73//Hs.116007:S79267
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559.94//Hs.29203:AI344105
- 50 R-MAMMA1000616//EST//0.071:169.60//Hs.144096:AI032180
 R-MAMMA1000621//ESTs//1.0e-90:477.94//Hs.26073:R96361
 R-MAMMA1000623
 R-MAMMA1000625//ESTs//3.4e-98:556.91//Hs.119482:AI361002
- 55 R-MAMMA1000643//EST//4.9e-74:379.96//Hs.137447:AA342203
 R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400.76//Hs.53531:AJ224162
 R-MAMMA1000669//EST//6.9e-53:368.84//Hs.149580:AI281881

- R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/8.4e-98:464:98//Hs.13431:AI022065
- R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476
- R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212
- 5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343
- R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644
- R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333
- R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/1.2e-29:158:79//Hs.142764:AA205569
- 10 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515
- R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329
- R-MAMMA1000723//Homo sapiens mRNA for alpha(2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942
- R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
- 15 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
- R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]/1.2e-35:371:74//Hs.141429:AA631915
- R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141
- R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.elegans]/2.3e-116:557:98//Hs.11472:AA632288
- 20 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205
- R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503
- R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
- R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
- 25 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
- R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353
- R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
- R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
- R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150
- 30 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163
- R-MAMMA1000802//Clathrin, light polypeptide (Lcb)/1.5e-45:358:76//Hs.73919:X81637
- R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675
- R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881
- R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902
- 35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/9.4e-44:363:79//Hs.96337:AA225358
- R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097
- R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955
- R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251
- 40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390
- R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212
- R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311
- R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922
- R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099
- 45 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399
- R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875
- R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243
- R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128
- R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166
- 50 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107
- R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215
- R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329
- R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093
- 55 R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634
- R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989
- R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

R-MAMMA1000931//ESTs//1.2e-80.457.91//Hs.122319:AA578233
R-MAMMA1000940//ESTs//3.3e-43.329.82//Hs.35254:AI133727
R-MAMMA1000941//ESTs//7.5e-55.306.84//Hs.163936:AA632281
R-MAMMA1000942//ESTs//7.2e-83.405.98//Hs.116491:AA650428
R-MAMMA1000943//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//9.3e-79.567:80//Hs.1361:M55053
R-MAMMA1000956//EST//5.7e-53.256:100//Hs.162209:AA536178
R-MAMMA1000957//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49.340.85//Hs.103458:X53795
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48.216.85//Hs.153468:AB011147
R-MAMMA1000968//EST//6.2e-46.302.86//Hs.149580:AI281881
R-MAMMA1000975//ESTs//1.4e-85.428.96//Hs.141742:W22204
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39.338.79//Hs.93121:AB018304
R-MAMMA1000987//EST//2.8e-41.249.90//Hs.149580:AI281881
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445.77//Hs.77579:AF013263
R-MAMMA1001003//Slalophorin (gpL15, leukosialin, CD43)//4.1e-51.282.82//Hs.80738:X52075
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82.405.97//Hs.25863:AA630313
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44.309.86//Hs.153563:AF011333
R-MAMMA1001024//ESTs//6.8e-35.333.78//Hs.107657:AA126814
R-MAMMA1001030//ESTs//1.6e-110.552.96//Hs.59483:AA524536
R-MAMMA1001035//ESTs//1.0e-45.273.85//Hs.138856:H47461
R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50.298.91//Hs.40100:AB002390
R-nnnnnnnnnnn//ESTs//3.6e-86.445.95//Hs.122625:R68650
R-MAMMA1001050//EST//2.2e-54.387.85//Hs.149580:AI281881
R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13.273.65//Hs.98738:AI015487
R-MAMMA1001067//ESTs//1.3e-38.324.78//Hs.20190:AA525532
R-MAMMA1001073//ESTs//5.2e-106.554.94//Hs.12336:W63748
R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38.544.68//Hs.153014:AB002353
R-MAMMA1001075//ESTs//2.0e-98.463.99//Hs.18341:N38944
R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84.556.85//Hs.23094:M19503
R-MAMMA1001082//ESTs//2.4e-71.356.97//Hs.152302:T90222
R-MAMMA1001091//ESTs//4.7e-83.429.95//Hs.154412:AA310926
R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34.262.82//Hs.129727:AF035587
R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27.232.76//Hs.61840:U28686
R-MAMMA1001110//ESTs//1.6e-17.128.87//Hs.161314:AI421576
R-MAMMA1001126//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//8.5e-43.462.78//Hs.16007:S79267
R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59.460.81//Hs.5247:AF029750
R-MAMMA1001139//ESTs//1.3e-62.341.94//Hs.18819:R01029
R-MAMMA1001143//ESTs//3.0e-48.383.80//Hs.152340:AA521399
R-MAMMA1001145//Calcium modulating ligand//5.1e-48.403.79//Hs.13572:AF068179
R-MAMMA1001154//EST//8.3e-35.313.75//Hs.162404:AA573131
R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58.409.84//Hs.5247:AF029750
R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91.430.99//Hs.129982:AI420970
R-MAMMA1001185//ESTs//5.0e-112.557.96//Hs.118181:W02251
R-MAMMA1001186//ESTs//3.8e-85.410.99//Hs.163811:W44959
R-MAMMA1001191//ESTs//0.018.57.87//Hs.141253:AA226519
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80.358.96//Hs.163827:AA074202
R-MAMMA1001202//ESTs//7.0e-43.230.95//Hs.79788:AA527348
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)/2.6e-65.348.79//Hs.73919:X81637
R-MAMMA1001206//EST//0.098.84.72//Hs.162941:AA635148

- R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
 R-MAMMA1001243//EST//0.09:143:62//Hs.68522:C20701
 5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
 15 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
 20 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
 25 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
 30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
 35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
 40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
 R-MAMMA1001465
 45 R-MAMMA1001476//Homo sapiens yeast sac permease-like molecule 3 (YSP3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522
 R-MAMMA1001510
 50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
 55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

- R-MAMMA1001604
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]/1.9e-97:488.96//Hs.143263:AI057616
- 5 R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408.76//Hs.121493:D25272
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472.76//Hs.15519:AB018315
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]/6.8e-15:168.73//Hs.115216:AA291074
R-MAMMA1001633//EST//5.1e-14:228.68//Hs.141456:N36377
R-MAMMA1001635//ESTs//3.4e-37:368.75//Hs.164033:AA769606
- 10 R-MAMMA1001649
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272.81//Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)/5.7e-50:304.89//Hs.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312.65//Hs.137153:R46248
- 15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation inhibitor 1//0.066:196.62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447.98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246.73//Hs.67619:AB007957
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294.89//Hs.3094:D31884
- 20 R-MAMMA1001711//ESTs//2.4e-86:439.96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399.9311//Hs.124620:AI082338
R-MAMMA1001730//ESTs//1.1e-85:403.99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]/3.7e-110:552.96//Hs.6923:AI161158
- 25 R-MAMMA1001740//ESTs//4.6e-45:342.82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412.85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374.84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375.73//Hs.139715:N25041
- 30 R-MAMMA1001754//EST//0.18:144.66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-9:8.488.96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206.86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434.58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299.85//Hs.149323:AB002325
- 35 R-MAMMA1001769//EST//1.7e-15:139.81//Hs.162399:AA572825
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.musculus]/7.6e-43:257.91//Hs.7634:AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272.86//Hs.73614:U83460
- 40 R-MAMMA1001785//ESTs//1.5e-87:431.98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108.62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340.80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297.84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446.98//Hs.129034:AA776892
- 45 R-MAMMA1001815//EST//0.00053:371.59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325.87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303.89//Hs.149580:AI281881
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438.75//Hs.32567:AF073519
- 50 R-MAMMA1001836//ESTs//3.8e-06:128.71//Hs.143611:M78140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339.83//Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125.85//Hs.161662:AA836811
R-MAMMA1001851//ESTs//4.5e-48:344.84//Hs.138856:H47461
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)/2.6e-38:280.83//Hs.155464:AF088219
- 55 R-MAMMA1001858//ESTs//1.1e-44:331.83//Hs.44702:AI148840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262.77//Hs.5737:AB007944
R-nnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450.58//Hs.132206:

AB014540

- R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696
R-MAMMA1002236
R-MAMMA1002243
- 5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0487//1.6e-54:207:81//Hs.92381:AB007956
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772
- 10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881
15 R-MAMMA1002297//ESTs//6.5e-45:323:63//Hs.155475:AA761454
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359
R-MAMMA1002308
20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/4.3e-49:457:76//Hs.144563:AF057280
- 25 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317
30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618
R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228
35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)/4.9e-31:217:88//Hs.73919:X81637
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
- 40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219
- 45 R-MAMMA1002385//ESTs//6.5e-203:63//Hs.146303:AA579061
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
50 R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488
R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475
R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348
- 55 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

- 89121:AB007954
 R-MAMMA1002461//ESTs//4.7e-111.548.97//Hs.104281:AA147076
 R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]/8.5e-104.544.93//Hs.94570:AI192106
- 5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/3.4e-31:263.79//Hs.38687:AA744496
 R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.0e-34:159.79//Hs.133526:N21103
- 10 R-MAMMA1002485//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds//8.9e-116.560.97//Hs.155223:AF055460
 R-MAMMA1002494//ESTs//3.2e-47.303.88//Hs.155243:N70293
 R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331.58//Hs.37035:U07664
- 15 R-MAMMA1002524//ESTs//0.0039:354.61//Hs.125797:AA806277
 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103.529.95//Hs.18858:AF065214
 R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50.317.88//Hs.153468:AB011147
- 20 R-MAMMA1002554//ESTs//2.3e-85.445.95//Hs.139140:AA218851
 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.0e-12:280.65//Hs.12725:T65058
 R-MAMMA1002566//ESTs//2.3e-88.421.99//Hs.17602:AA705681
 R-MAMMA1002571//ESTs//5.1e-97.456.99//Hs.152834:AA595693
 R-MAMMA1002573//ESTs//3.1e-38.258.87//Hs.163989:R74433
- 25 R-MAMMA1002585//ESTs//7.8e-96.533.91//Hs.26009:H49371
 R-MAMMA1002590//ESTs//0.61:202.62//Hs.161190:AI419258
 R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177.75//Hs.1360:M29874
 R-MAMMA1002598//ESTs//3.4e-113.544.97//Hs.20263:AA573737
- 30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225.80//Hs.51124:AF019369
 R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46.424:75//Hs.1361:M55053
 R-MAMMA1002617//ESTs//1.1e-38.229.92//Hs.96987:W27389
- 35 R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185.73//Hs.108287:L27670
 R-MAMMA1002619//ESTs//1.7e-95.480.96//Hs.54873:AA526306
 R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298.87//Hs.89887:D38081
 R-MAMMA1002623//EST//4.3e-49:336.85//Hs.149580:AI281881
 R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]/2.3e-35:308.79//Hs.93332:AA811920
- 40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283.86//Hs.115325:D84488
 R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303.89//Hs.40100:AB002390
 R-MAMMA1002637//ESTs//1.3e-55:391.85//Hs.95074:AI144421
 R-MAMMA1002646//ESTs//7.4e-36:182.80//Hs.163937:N69915
- 45 R-MAMMA1002650//ESTs//1.6e-102:547.94//Hs.57841:W63776
 R-MAMMA1002655
 R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462.75//Hs.97476:AB007886
 R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376.82//Hs.154326:D42087
 R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]/5.3e-108.544:96//Hs.16464:W19606
- 50 R-MAMMA1002673//EST//3.3e-35:169.79//Hs.140046:AA668213
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544.96//Hs.3363:D86987
 R-MAMMA1002685//EST//1.9e-31:223.86//Hs.112540:AA601385
- 55 R-MAMMA1002698//ESTs//5.9e-43:292.85//Hs.144660:AA652675
 R-MAMMA1002699//ESTs//3.2e-25:134.100//Hs.126049:F22510
 R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/6.9e-70:353.96//Hs.138404:R70986

- R-MAMMA1002708//ESTs//2.1e-76:413.94//Hs.57932:W69234
 R-MAMMA1002711//ESTs//1.9e-44:236.96//Hs.138575:H67858
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273.89//Hs.153563:AF011333
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)/3.4e-42:266.88//Hs.155464:AF088219
 R-MAMMA1002744//ESTs//4.2e-18:473.63//Hs.42826:AA846757
 R-MAMMA1002746//ESTs//1.8e-100:473.99//Hs.117558:AA779907
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330.80//Hs.154069:U06452
 10 R-MAMMA1002754//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369.77//Hs.105292:AA504776
 R-MAMMA1002758
 R-MAMMA1002764//ESTs//4.2e-103:486.99//Hs.159909:AI393281
 R-MAMMA1002765//ESTs//1.6e-37:338.76//Hs.37573:H59651
 15 R-MAMMA1002769//ESTs//0.72:409.57//Hs.141376:AI301272
 R-MAMMA1002780//ESTs//1.6e-52:292.92//Hs.135985:AA342750
 R-MAMMA1002782//ESTs//1.0e-31:157.80//Hs.159510:AA297145
 R-MAMMA1002796//ESTs//3.8e-49:284.92//Hs.156479:AA513812
 R-MAMMA1002807//Archaeal//1.4e-39:315.80//Hs.33642:X81198
 20 R-MAMMA1002820//ESTs//5.0e-14:192.74//Hs.134635:AA226260
 R-MAMMA1002830//EST//4.0e-50:255.97//Hs.160674:AI248319
 R-MAMMA1002833//EST//1.2e-48:306.88//Hs.149580:AI281881
 R-MAMMA1002835
 R-MAMMA1002838//EST//2.7e-12:161.76//Hs.163252:AA828723
 25 R-MAMMA1002842//ESTs//1.7e-41:366.78//Hs.141899:N22395
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258.79//Hs.78160:AF010238
 R-MAMMA1002844//ESTs//3.5e-51:250.99//Hs.151445:AA351081
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361.91//Hs.85155:X79067
 R-MAMMA1002868//ESTs//2.1e-38:301.80//Hs.132717:AA171941
 30 R-MAMMA1002871//EST//6.0e-88:413.99//Hs.149057:AI243592
 R-MAMMA1002880//ESTs//6.5e-100:506.96//Hs.163533:N52194
 R-MAMMA1002881//EST//1.1e-40:335.80//Hs.160895:AI365871
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)/3.4e-36:228.88//Hs.155464:AF088219
 R-MAMMA1002887//ESTs//4.7e-67:409.99//Hs.152155:AA424811
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322.80//Hs.26929:AF008915
 R-MAMMA1002895//ESTs//2.7e-32:330.76//Hs.139132:AA211087
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313.86//Hs.13572:AF068179
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132.76//Hs.90981:D80002
 R-MAMMA1002930//EST//4.9e-44:260.91//Hs.149580:AI281881
 R-MAMMA1002938
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556.85//Hs.23094:M19503
 R-MAMMA1002947//ESTs//7.0e-22:222.80//Hs.103395:T79243
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427.77//Hs.153014:AB002353
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300.84//Hs.89887:D38081
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525.95//Hs.94396:AA399630
 R-MAMMA1002973//ESTs//4.4e-40:257.87//Hs.163580:H15835
 R-MAMMA1002982//ESTs//2.5e-28:115.87//Hs.141694:W15279
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402.67//Hs.133089:AF064019
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380.79//Hs.13572:AF068179
 R-MAMMA1003004//ESTs//3.0e-07:378.60//Hs.61885:AI127857
 R-MAMMA1003007//ESTs//2.0e-47:404.80//Hs.146314:R99617
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320.90//Hs.92023:AI022248
 R-MAMMA1003015//ESTs//1.5e-42:363.79//Hs.155184:AA573189
 R-MAMMA1003019//ESTs//4.8e-10:232.66//Hs.111341:AA251268

- R-MAMMA1003026//ESTs//2.3e-63:394.99//Hs.24668:AA897315
 R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358
- 5 R-MAMMA1003035//ESTs//1.3e-94:481.94//Hs.92411:AA603321
 R-MAMMA1003039//EST//0.56:210.61//Hs.162248:AA552160
 R-MAMMA1003040//ESTs//2.1e-17:261.70//Hs.46980:W55940
 R-MAMMA1003044//EST//2.4e-18:124.91//Hs.130321:AI002941
 R-MAMMA1003047//ESTs//1.0e-20:209.78//Hs.15916:H12862
 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184.60//Hs.2510:X57348
- 10 R-MAMMA1003055//EST//1.0e-49:281.92//Hs.149580:AI281881
 R-MAMMA1003056//ESTs//0.99:107.66//Hs.30348:AI038559
 R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545.93//Hs.13755:AA878911
 R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322.83//Hs.66710:X96969
- 15 R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421.70//Hs.161959:AA493652
 R-MAMMA1003099//ESTs//1.1e-43:379.79//Hs.37573:H59651
 R-MAMMA1003104//ESTs//2.1e-97:498.96//Hs.9299:T51283
 R-MAMMA1003113//EST//3.7e-29:457.70//Hs.123616:AA815366
- 20 R-MAMMA1003127//ESTs//2.6e-41:283.86//Hs.146811:AA410788
 R-MAMMA1003135//ESTs//7.2e-101:504.97//Hs.87729:AA863125
 R-MAMMA1003140//ESTs//4.3e-44:200.89//Hs.152093:AI149537
 R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413.61//Hs.152213:L20861
- 25 R-nnnnnnnnnnnnn
 R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524.89//Hs.6884:W30736
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587.94//Hs.108112:AF070640
 R-NT2RM4000024//ESTs//2.9e-98:523.94//Hs.26641:R59312
- 30 R-NT2RM4000027
 R-NT2RM4000030//ESTs//1.6e-96:482.96//Hs.90625:T03663
 R-NT2RM4000046//ESTs//1.6e-91:461.97//Hs.151237:AI86169
 R-NT2RM4000061//ESTs//4.3e-31:167.97//Hs.110821:Z78379
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549.97//Hs.95665:AF070639
- 35 R-NT2RM4000086//EST//2.7e-17:212.76//Hs.137041:AA877817
 R-NT2RM4000104//ESTs//3.0e-85:452.94//Hs.101750:H19708
 R-NT2RM4000139//EST//3.3e-05:156.66//Hs.133228:AI052312
 R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536.92//Hs.127810:AI246301
- 40 R-NT2RM4000156//EST//0.89:169.62//Hs.162967:AA676397
 R-nnnnnnnnnnnnn//ESTs//1.0:214.61//Hs.119370:W52962
 R-NT2RM4000169//ESTs//5.4e-82:440.93//Hs.159379:AI382160
 R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542.93//Hs.6366:AA614113
- 45 R-NT2RM4000197//ESTs//5.4e-113:567.96//Hs.22975:AA156723
 R-NT2RM40001991ESTs//10.020:95.651Hs.146203:AI254528
 R-NT2RM4000200//ESTs//1.4e-100:488.97//Hs.126538:AA931876
 R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330.77//Hs.155464:AF088219
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546.94//Hs.111138:AB018255
- 50 R-NT2RM4000215
 R-nnnnnnnnnnnnn//ESTs//7.1e-92:457.97//Hs.162074:AA477760
 R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174.66//Hs.235.X51602
- 55 R-NT2RM4000244//ESTs//6.6e-61:320.95//Hs.108646:AA613031
 R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219.62//Hs.119498:AF000974
 R-NT2RM4000265//ESTs//8.8e-105:489.99//Hs.131001:AI378742

- R-NT2RM4000290//ESTs//4.0e-87.435.96//Hs.162592:AA594128
 R-NT2RM4000324//ESTs//2.2e-80.413.96//Hs.12313:R43673
 R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45.286.87//Hs.155464:AF088219
 R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60.452.84//Hs.73919:X81637
 5 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117.579.96//Hs.5216:AA534881
 R-NT2RM4000354//ESTs//2.1e-85.406.99//Hs.126774:AI224479
 R-NT2RM4000356//ESTs//7.9e-109.548.96//Hs.44278:AA418063
 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113.577.95//Hs.8152:AB014542
 R-NT2RM4000368//ESTs//2.2e-61.310.97//Hs.143611:M78140
 10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93.521.92//Hs.41793:AA775879
 R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99.524.94//Hs.5249:U55977
 R-NT2RM4000414//EST//2.7e-06.196.64//Hs.136648:AA688285
 15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75.470.90//Hs.69235:AA192359
 R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112.69//Hs.19949:X98173
 R-NT2RM4000433//ESTs//2.7e-100.479.98//Hs.24553:AI150687
 R-NT2RM4000457//ESTs//5.1e-107.535.95//Hs.7579:AA775865
 20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492.96//Hs.21090:AA418587
 R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102.493.97//Hs.111279:W84558
 R-NT2RM4000496
 25 R-NT2RM4000511//EST//5.1e-43.326.81//Hs.157658:AI358465
 R-NT2RM4000514//ESTS//1.7e-112.552.96//Hs.6686:AA205496
 R-nnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60.343.93//Hs.16014:AA074879
 R-NT2RM4000520//ESTs//2.7e-55.266.100//Hs.99838:AA204731
 30 R-NT2RM4000531//ESTs//2.0e-88.502.91//Hs.13110:T67461
 R-NT2RM4000532//ESTs//0.47:290.58//Hs.148753:T91777
 R-NT2RM4000534//EST//0.00025.303.60//Hs.162809:AA632198
 R-NT2RM4000585//EST//0.28.63.77//Hs.150024:AI291981
 R-NT2RM4000590//ESTs//5.8e-65.320.98//Hs.116017:AA613437
 35 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189.64//Hs.16349:AB007891
 R-NT2RM4000603//ESTs//4.6e-68.356.96//Hs.48855:AA134589
 R-nnnnnnnnnnn//ESTs//1.5e-89.431.97//Hs.26117:W16697
 R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:519.96//Hs.14779:N64822
 40 R-NT2RM4000674//ESTs//5.1e-78.398.97//Hs.8268:N70144
 R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115.550.98//Hs.11820:AA205531
 R-NT2RM4000698//ESTs//2.0e-17.130.87//Hs.86420:AA927510
 R-nnnnnnnnnnn
 R-NT2RM4000712//EST//0.99:103.65//Hs.114039:AA701128
 45 R-NT2RM4000711//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103.519.95//Hs.6823:W18181
 R-NT2RM4000733//ESTs//8.7e-88.429.98//Hs.72185:AA465311
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105.536.95//Hs.137168:AB018303
 50 R-NT2RM4000741//ESTs//0.99:266.58//Hs.142718:AA034046
 R-NT2RM4000751//ESTs//1.6e-20.351.66//Hs.43145:AA776988
 R-NT2RM4000764
 R-NT2RM4000778//EST//0.066.254.61//Hs.148232:AA904174
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106.546.94//Hs.18586:AB007920
 55 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40.424.73//Hs.154069:U06452
 R-NT2RM4000790//EST//9.0e-48.259.94//Hs.156964:AI417008

- R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891
 R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868
- 5 R-NT2RM4000813
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:AI219667
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031
- 10 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864
 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597
 R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343
 R-ntnnnnnnnnnn
 R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514
- 15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262
 R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887
 R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647
 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126
- 20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539
 R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352
- 25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132
 R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300
 R-ntnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W2798
 R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324
- 30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962
 R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276
 R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311
 R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848
 R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085
- 35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174
 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942
 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849
 R-NT2RM4001203
- 40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184
 R-NT2RM4001309
- 45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.18442:AI129307
- 50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339
 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476
 R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211
 R-NT2RM4001382
- 55 R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507
 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790
 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:94//Hs.15744:AI055859
 R-NT2RM4001412

- R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895
 R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812
- 5 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277
 R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585
- 10 R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664
 R-NT2RM40015227//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219
 R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:HA3072
 R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027
 R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-Kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046
- 15 R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009
 R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946
- 20 R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171
 R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871
 R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334
- 25 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079
 R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957
 R-NT2RM4001650
 R-NT2RM4001662
 R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938
- 30 R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496
 R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440
 R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686
 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887
- 35 R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390
 R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200
 R-NT2RM4001754//Human kpni repeat mna (cdna clone cpd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629
 R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740
 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270
 R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956
 R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567
- 40 R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920
 R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
 R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
 R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
 R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
- 50 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
 R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
 R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
 R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
 R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
- 55

- R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
- 5 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143
 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
- 10 R-ntnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265
 R-NT2RM4001984
 R-NT2RM4001987
 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528
- 15 R-NT2RM4002018
 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087
 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435
 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T87226
 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887
- 20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179
 R-ntnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309
 R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629
 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416
- 25 R-NT2RM4002075//EST//0.078:267:61//Hs.163563:AA641655
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528
 R-ntnnnnnnnnnn//ESTs//1.0e-95:69//Hs.25897:W65409
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620
- 30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987
 R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535
- 35 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258
 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
- 40 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219
- 45 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA1128263
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
 R-NT2RM4002294
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164
- 50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
 R-ntnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549
- 55 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884
 R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

- 98//Hs.16464:W19606
 R-NT2RM4002438//ESTs//0.74:162.61//Hs.65377:AA994677
 R-NT2RM4002446
 R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142
 R-NT2RM4002457
 R-NT2RM4002460//ESTs//3.0e-74:385.96//Hs.6933:R07890
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507.97//Hs.8765:AF083255
 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172.98//Hs.94781:AB014591
 R-NT2RM4002493//ESTs//6.4e-73:366.97//Hs.157114:T58884
 R-NT2RM4002499//ESTs//3.5e-61:307.97//Hs.117737:AI088029
 R-NT2RM4002504//ESTs//2.1e-55:306.94//Hs.10949:AA464464
 R-nnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360.91//Hs.31030:H50467
 R-NT2RM4002532//ESTs//1.3e-21:191.78//Hs.146811:AA410788
 R-NT2RM4002534//ESTs//1.8e-99:512.95//Hs.13526:AI417057
 R-NT2RM4002567//ESTs//7.6e-41:272.87//Hs.7114:R24312
 R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGLACETOSAMINYLTRANSFERASE [Bos taurus]//2.3e-89:435.97//Hs.15830:AA165698
 R-NT2RM4002593//ESTs//2.3e-109:552.96//Hs.17424:AA190569
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//9.6e-28:194.87//Hs.59346:AI126802
 R-NT2RP2000001//ESTs//2.6e-80:386.99//Hs.105061:N45096
 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253.84//Hs.89887:D38081
 R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366.67//Hs.54488:X69115
 R-NT2RP2000027//ESTs//9.5e-74:377.96//Hs.96557:AA286713
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223.96//Hs.8309:AB018290
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309.98//Hs.6216:AF061749
 R-NT2RP2000054//EST//1.2e-71:375.96//Hs.98835:AA435798
 R-NT2RP2000056//EST//2.8e-28:342.69//Hs.135526:AI094910
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199.94//Hs.41793:AA775879
 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383.98//Hs.58254:W72881
 R-NT2RP2000076//EST//0.0014:227.63//Hs.136761:AA738097
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379.97//Hs.54877:AF050078
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232.75//Hs.102576:AJ010230
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378.96//Hs.22926:AB018338
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236.63//Hs.41:D90064
 R-NT2RP2000097//ESTs//4.2e-15:92.97//Hs.7432:AA281757
 R-NT2RP2000098//ESTs//9.0e-53:279.94//Hs.87807:AA813827
 R-NT2RP2000108//EST//1.5e-75:378.96//Hs.162105:AA524419
 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386.95//Hs.17706:AB018356
 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153.86//Hs.5268:W22670
 R-nnnnnnnnnnn//ESTs//1.0e-55:293.95//Hs.14570:AI422099
 R-nnnnnnnnnnn//ESTs//0.24:354.59//Hs.157564:AI356513
 R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457.95//Hs.3832:AI208601
 R-NT2RP2000153//EST//0.0039:93.68//Hs.140386:AA773548
 R-NT2RP2000157//ESTs//1.1e-53:322.91//Hs.6877:AA040820
 R-NT2RP2000161//EST5//1.6e-99:492.97//Hs.21738:AI188190
 R-NT2RP2000175//ESTs//1.4e-98:489.96//Hs.4849:AI143741
 R-NT2RP2000183//ESTs//9.0e-72:358.96//Hs.4856:N51373
 R-NT2RP2000195//ESTs//3.9e-92:439.98//Hs.145091:AA814510

- R-NT2RP2000205//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.4e-80:415:95//Hs.11807:T86897
- R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)/1.1e-57:306:94//Hs.79402:AC004382
- R-NT2RP2000232
- 5 R-NT2RP2000233//ESTs/1.1e-08:63:96//Hs.124861:AI090683
- R-NT2RP2000239//ESTs/5.3e-87:427:96//Hs.86211:AA604379
- R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]/1.3e-95:454:99//Hs.102057:AA649005
- R-NT2RP2000257//ESTs/5.1e-58:282:99//Hs.122565:AI126840
- 10 R-NT2RP2000258//EST/1.0:67:68//Hs.61812:AA035649
- R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/8.4e-59:298:96//Hs.16085:AI261382
- R-NT2RP2000274//ESTs/7.5e-61:296:98//Hs.86081:AA196635
- R-NT2RP2000288//ESTs/1.8e-56:305:93//Hs.7579:AA775865
- 15 R-NT2RP2000289
- R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]/9.8e-106:494:99//Hs.102951:AA574249
- R-NT2RP2000298//ESTs/2.1e-62:256:90//Hs.8737:W22712
- R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds/2.8e-39:222:93//Hs.58218:U82381
- 20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs/2.9e-71:342:98//Hs.87684:AL022398
- 25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]/3.4e-69:371:94//Hs.43436:N32441
- R-NT2RP2000337//ESTs/5.2e-79:411:95//Hs.101799:AI276062
- R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds/1.1e-47:262:94//Hs.76556:U83981
- 30 R-NT2RP2000369//ESTs/4.3e-102:531:94//Hs.15855:H98103
- R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds/8.4e-09:93:83//Hs.808:L28010
- R-NT2RP2000420//ESTs/8.2e-24:142:94//Hs.144893:AI222324
- R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds/4.2e-20:140:90//Hs.5819:AF102265
- 35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]/1.3e-65:362:93//Hs.22197:AI151425
- R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]/3.6e-75:435:92//Hs.21938:W81045
- R-NT2RP2000459//ESTs/2.8e-95:527:93//Hs.103422:AI352013
- R-NT2RP2000498//ESTs/2.3e-17:119:79//Hs.161714:AA229078
- 40 R-NT2RP2000503//ESTs/5.2e-91:438:98//Hs.152335:AI290215
- R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds/0.13:455:58//Hs.110:AB007896
- R-nnnnnnnnn//ESTs/9.9e-63:376:89//Hs.47546:AA181348
- R-NT2RP2000523
- R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds/3.5e-30:167:97//Hs.14409:AB011144
- 45 R-NT2RP2000617//ESTs/9.5e-103:493:98//Hs.9412:W72446
- R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds/8.1e-66:335:96//Hs.7314:AB014514
- R-NT2RP2000644//ESTs/1.1e-18:372:63//Hs.82419:AA789222
- R-NT2RP2000656//ESTs/1.0e-10:128:80//Hs.23977:AA115275
- R-NT2RP2000658//ESTs/0.31:278:59//Hs.15661:W02396
- 50 R-NT2RP2000668//ESTs/8.2e-40:255:88//Hs.113310:R16767
- R-NT2RP2000678//ESTs/2.6e-53:271:9611Hs.23790:N99347
- R-NT2RP2000710//ESTs/0.49:190:63//Hs.145521:AI261368
- R-NT2RP2000715//EST/1.1e-87:418:9911Hs.139425:AA429279
- R-NT2RP2000731//EST/5.3e-65:322:97//Hs.136754:AA713965
- 55 R-NT2RP2000758//ESTs/1.0:187:61//Hs.10545:N62642
- R-NT2RP2000764//ESTs/5.8e-84:485:91//Hs.121816:AA775419
- R-NT2RP2000809
- R-NT2RP2000812//ESTs/1.2e-45:231:97//Hs.121028:AA902745

- R-nnnnnnnnnnnnn/ESTs//6.3e-87:433.97//Hs.145479:AA969404
 R-NT2RP2000816//ESTs//0.45:100.69//Hs.147529:AA458918
 R-NT2RP2000819
- 5 R-NT2RP2000841//ESTs//1.9e-73:351.99//Hs.116385:AI224511
 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6
 PRECURSOR//4.6e-10:247.66//Hs.29352:M31165
 R-NT2RP2000845//ESTs//2.8e-91:443.97//Hs.66810:AI206552
 R-NT2RP2000863//ESTs//4.3e-49:310.88//Hs.104336:W07345
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277.89//Hs.3615:
- 10 AB018284
 R-NT2RP2000892//ESTs//2.8e-50:25.8:96//Hs.119238:AA476267
 R-NT2RP2000931//MATRIN 3//7.2e-57:290.96//Hs.78825:AB018266
 R-NT2RP2000938//ESTs. Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III
 [Caenorhabditis elegans]//3.9e-37:199.95//Hs.112318:AA186477
- 15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494.96//Hs.19822:
 AB018298
 R-NT2RP2000965//EST//0.22:223.60//Hs.105703:AA487021
 R-NT2RP2000970//EST//8.7e-06:255.62//Hs.149202:AI246481
 R-NT2RP2000985//ESTs. Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC
 REGION [S. cerevisiae]//7.8e-92:468.95//Hs.12124:AA522537
- 20 R-NT2RP2000987//ESTs//4.5e-78:419.93//Hs.21968:H97521
 R-NT2RP2001036//EST//2.0e-33:148.82//Hs.163196:AA767643
 R-NT2RP2001044//ESTs//5.6e-95:493.95//Hs.21958:AA453660
 R-NT2RP2001065//ESTs//3.6e-28:153.96//Hs.119314:AA432108
- 25 R-NT2RP2001070//EST//0.30:94.67//Hs.94289:N73665
 R-NT2RP2001094//EST//0.75:101.69//Hs.161040:H82068
 R-NT2RP2001119
 R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304.94//Hs.146282:AB015348
 R-NT2RP2001137
- 30 R-NT2RP2001149//ESTs//5.1e-66:324.9711Hs.27475:AA704512
 R-NT2RP2001168//ESTs//2.0e-98:539.92//Hs.77870:AI188145
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490.96//Hs.26247:
 AB007949
 R-NT2RP2001174//ESTs//2.2e-63:354.93//Hs.24266:R28287
- 35 R-NT2RP2001196//ESTs//1.4e-83:463.93//Hs.124304:AA825510
 R-NT2RP2001218//ESTs//1.4e-100:506.96//Hs.93391:AI188402
 R-NT2RP2001226//EST//0.0074:154.63//Hs.128612:AA909358
 R-NT2RP2001233//ESTs. Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538.80//
 Hs.44014:AA632298
- 40 R-NT2RP2001245//ESTs//5.2e-90:447.97//Hs.14559:H92996
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544.97//Hs.7531:AB018353
 R-NT2RP2001277//ESTs//2.0e-81:387.99//Hs.13751:AA908229
 R-NT2RP2001290//ESTs//2.4e-91:501.92//Hs.12600:AA044775
 R-NT2RP2001295//ESTs//1.4e-70:337.99//Hs.123854:AA412665
- 45 R-NT2RP2001312//ESTs//4.6e-53:276.95//Hs.7961:AA401205
 R-NT2RP2001327//ESTs. Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H. sapiens]//
 2.3e-43:238.93//Hs.106632:N25679
 R-NT2RP2001328//ESTs//5.1e-99:499.96//Hs.34868:AI341138
 R-NT2RP2001347//ESTs//6.7e-05:100.77//Hs.9536:AA114178
- 50 R-NT2RP2001378//ESTs//4.2e-83:456.93//Hs.10554:N50028
 R-NT2RP2001381//ESTs//1.1e-26:148.96//Hs.161859:AA444038
 R-NT2RP2001392//ESTs. Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.
 sapiens]//3.9e-74:411.93//Hs.47305:AA195153
 R-NT2RP2001394//ESTs//9.5e-54:305.93//Hs.70256:R07875
 R-NT2RP2001397//ESTs. Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:
- 55 469.97//Hs.20483:AA522505
 R-NT2RP2001420//ESTs//1.6e-49:228.88//Hs.163602:N32030
 R-NT2RP2001423//ESTs//2.0e-37:190.99//Hs.101565:R35431

- R-NT2RP2001427//EST//1.7e-1 1:107.84//Hs.148584:AI201728
 R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558.97//Hs.7627:AI341556
 R-NT2RP2001440//EST//0.17:192.58//Hs.133442:AI061394
 R-NT2RP2001445//ESTs//1.1e-43:215.100//Hs.145497:AA501453
 5 R-NT2RP2001449//ESTs//4.1e-08:234.61//Hs.134067:AI076765
 R-NT2RP2001450//ESTs//9.5e-65:356.94//Hs.61829:AI079539
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255.83//Hs.155464:AF088219
 R-NT2RP2001506//ESTs//2.9e-23:170.88//Hs.7147:T23513
 R-NT2RP2001511//ESTs//2.0e-08:59.100//Hs.57660:AA251146
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545.95//Hs.4277:Y14494
 R-NT2RP2001526//ESTs//3.7e-23:295.72//Hs.8514:AF039240
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99.95//Hs.99742:AF035586
 15 R-NT2RP2001560//ESTs//2.2e-58:310.94//Hs.87454:AA732816
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387.96//Hs.67619:AB007957
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193.60//Hs.119:D14661
 R-NT2RP2001581//ESTs//5.1e-08:107.78//Hs.157114:T58884
 20 R-NT2RP2001597//EST//5.2e-22:151.88//Hs.158613:AI369995
 R-NT2RP2001601//ESTs//1.5e-78:373.99//Hs.137558:AI393767
 R-NT2RP2001613
 R-NT2RP2001628//EST//0.99:195.60//Hs.144238:W52294
 R-NT2RP2001663//ESTs//4.0e-37:282.84//Hs.12319:W56090
 25 R-NT2RP2001677//ESTs//1.4e-44:232.96//Hs.159387:AI370845
 R-NT2RP2001678//ESTs//0.91:124.60//Hs.10593:AI201336
 R-NT2RP2001699//EST//0.0033:230.61//Hs.146544:AI125323
 R-NT2RP2001720//ESTs//1.8e-52:255.99//Hs.101064:AA290579
 R-NT2RP2001721//ESTs//7.0e-101:479.99//Hs.129750:AA987538
 30 R-NT2RP2001740//ESTs//3.3e-76:379.96//Hs.144704:AI147100
 R-NT2RP2001748//ESTs//1.4e-44:352.81//Hs.142259:AA828840
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519.96//Hs.47504:AF091754
 R-NT2RP2001813//ESTs//6.3e-78:406.95//Hs.21902:R44037
 35 R-NT2RP2001861
 R-NT2RP2001869//EST//2.8e-21:173.82//Hs.130321:AI002941
 R-NT2RP2001876//ESTs//6.1e-102:526.95//Hs.4944:AA533088
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556.95//Hs.23159:AA113849
 40 R-NT2RP2001900//ESTs//6.9e-85:442.95//Hs.154220:AA171724
 R-NT2RP2001907//ESTs//2.1e-82:432.94//Hs.142257:AA1188423
 R-NT2RP2001926//EST//2.3e-24:299.71//Hs.135085:AI097268
 R-NT2RP2001936//ESTs//1.1e-45:265.92//Hs.112482:T66087
 R-NT2RP2001943//EST//1.4e-05:246.61//Hs.144096:AI032180
 45 R-NT2RP2001946//ESTs//3.6e-87:410.99//Hs.20242:W72594
 R-NT2RP2001947//ESTs//1.9e-55:338.88//Hs.58582:T72588
 R-NT2RP2001969
 R-NT2RP2001976//ESTs//1.2e-98:499.95//Hs.121028:AA902745
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118.89//Hs.18760:AA166678
 50 R-NT2RP2002025//ESTs//2.1e-82:393.98//Hs.159488:AI378233
 R-NT2RP2002032//ESTs//4.4e-98:531.91//Hs.93836:AA813332
 R-NT2RP2002033//ESTs//3.5e-43:229.96//Hs.30563:AA102627
 R-NT2RP2002041
 55 R-NT2RP2002046//ESTs//1.6e-101:476.99//Hs.101107:AA825938
 R-NT2RP2002047//ESTs//9.1e-85:431.95//Hs.116750:AA629895
 R-NT2RP2002058//ESTs//1.3e-31:163.99//Hs.33085:AA258068
 R-NT2RP2002066//ESTs//1.9e-87:459.93//Hs.118871:AA846091

- R-NT2RP2002070//ESTs//4.1e-63.332.96//Hs.156446:T92265
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26.178.87//Hs.11039.AF052183
 R-NT2RP2002079//ESTs//1.2e-79.389.97//Hs.135214:AI350524
 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60.376.89//Hs.155218:AJ007509
- 5 R-NT2RP2002105//ESTs//3.4e-54.313.90//Hs.98702:AI123000
 R-NT2RP2002124//ESTs//6.6e-81.431.93//Hs.127326:AA525134
 R-NT2RP2002137//Deoxycytidine kinase//0.29.183.62//Hs.709:M60527
 R-NT2RP2002154//ESTs//9.6e-97.539.91//Hs.18624:AA523268
- 10 R-NT2RP2002172//EST//0.69.53.75//Hs.156238:AI334495
 R-NT2RP2002185//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.4e-54.269.98//Hs.107201:W52859
 R-NT2RP2002192//ESTs. Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-15.245.71//Hs.87578:AI125363
 R-NT2RP2002193//ESTs//3.5e-79.45.3.90//Hs.76578:AI290672
- 15 R-NT2RP2002208//ESTs//2.0e-72.347.99//Hs.164028:AI003946
 R-NT2RP2002219//EST//0.039.229.63//Hs.149830:AI287499
 R-NT2RP2002231//ESTs//3.3e-64.337.94//Hs.79828:AA642341
 R-nnnnnnnnnnn//ESTs. Highly similar to co-repressor protein [M.musculus]//5.4e-48.238.99//Hs.22583:AA188168
- 20 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15.131.83//Hs.150595:AF005418
 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99.548.91//Hs.92137:M19720
 R-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100.550.91//Hs.4029:Z78373
 R-NT2RP2002292//ESTs. Weakly similar to F13B12.1 [C.elegans]//3.2e-92.482.93//Hs.5570:AI377963
- 25 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103.527.94//Hs.24812:AF069532
 R-NT2RP2002316//ESTs//4.2e-91.425.100//Hs.3350:AI368015
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112.567.95//Hs.31034:AB015594
- 30 R-NT2RP2002333//ESTs//1.9e-86.483.91//Hs.155198:AA767372
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103.600.89//Hs.109051:AF038958
 R-NT2RP2002394//ESTs//0.11.158.65//Hs.28792:AI343467
 R-NT2RP2002408//ESTs//1.5e-51.278.93//Hs.6044:W22815
- 35 R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33.285.80//Hs.15731:AB011135
 R-NT2RP2002439//ESTs//3.2e-12.134.76//Hs.32246:AA464020
 R-NT2RP2002457//ESTs//4.7e-52.282.94//Hs.21968:H97521
 R-NT2RP2002464//ESTs//5.3e-27.148.98//Hs.115660:AI362230
- 40 R-NT2RP2002475//ESTs//3.9e-85.439.94//Hs.9873:W27233
 R-nnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115.605.92//Hs.125856:AB005289
 R-NT2RP2002498//ESTs//6.3e-37.227.93//Hs.108779:N73180
 R-NT2RP2002503//ESTs//1.9e-54.358.86//Hs.57800:W60838
- 45 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107.583.91//Hs.23255:AB018334
 R-NT2RP2002520//ESTs//4.2e-99.509.94//Hs.32368:AA205305
 R-NT2RP2002537//ESTs//4.2e-105.552.93//Hs.154363:AA533090
 R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109.570.93//Hs.49476:AF009314
- 50 R-NT2RP2002549//DNA polymerase gamma//1.1e-35.189.86//Hs.80961:U60325
 R-NT2RP2002591//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118.564.97//Hs.94549:AA149547
 R-NT2RP2002595//EST//1.4e-15.101.95//Hs.129528:AA994783
 R-NT2RP2002606//ESTs//4.5e-99.475.98//Hs.45046:N40170
- 55 R-NT2RP2002609//ESTs//1.9e-104.568.92//Hs.9175:AI184220
 R-NT2RP2002618//ESTs//0.014.493.57//Hs.96322:AA541615
 R-NT2RP2002621//EST//4.4e-36.252.84//Hs.149580:AI281881
 R-NT2RP2002643//ESTs//6.9e-32.247.74//Hs.33354:AA179944

- R-NT2RP20020672
 R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184.63//Hs.50727:U43572
 R-NT2RP2002706//EST//2.8e-41:148.86//Hs.161917:AA483223
 R-NT2RP2002710//EST//0.34:105.71//Hs.136747:AA749210
 5 R-NT2RP2002727//ESTs//8.7e-68:368.94//Hs.14366:T78626
 R-NT2RP2002736//ESTs//9.7e-98:457.99//Hs.74899:AA993300
 R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360.59//Hs.119139:AB011108
 R-NT2RP2002741//ESTs//3.1e-102:489.98//Hs.112024:AI042352
 R-NT2RP2002750//EST//3.6e-43:166.86//Hs.162404:AA573131
 10 R-NT2RP2002752//ESTs//5.0e-56:355.89//Hs.95867:M62042
 R-NT2RP2002753//ESTs//1.7e-49:262.96//Hs.49005:W89124
 R-NT2RP2002769//ESTs//1.3e-59:376.88//Hs.4046:H03587
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341.94//Hs.17481:AF070537
 R-NT2RP2002800//ESTs//6.5e-08:79.84//Hs.153262:AA551124
 15 R-NT2RP2002839//ESTs. Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501.97//Hs.136202:AA206578
 R-NT2RP2002857//ESTs//4.3e-94:463.97//Hs.134292:AA603031
 R-NT2RP2002862//ESTs//2.3e-42:302.82//Hs.117969:H94870
 R-NT2RP2002880
 20 R-NT2RP2002891
 R-NT2RP2002925//ESTs//1.3e-103:564.92//Hs.142079:AA182894
 R-NT2RP2002928//ESTs//3.9e-108:502.99//Hs.29105:AA574143
 R-NT2RP2002929//ESTs//4.1e-106:499.99//Hs.44743:AA837096
 R-NT2RP2002954//ESTs//2.6e-88:417.99//Hs.100824:AI308771
 25 R-NT2RP2002959//ESTs//7.5e-101:489.97//Hs.32690:N57480
 R-NT2RP2002979//ESTs//5.4e-06:197.65//Hs.146726:AI147060
 R-NT2RP2002980//ESTs//1.0e-110:562.96//Hs.28444:AA083213
 R-NT2RP2002986//ESTs. Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578.97//Hs.106290:AI125291
 30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78.74//Hs.146395:AB002329
 R-NT2RP2002993//ESTs. Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467.98//Hs.86337:AA149311
 R-NT2RP2003000//ESTs//0.0070:400.61//Hs.138506:U85642
 R-NT2RP2003034//ESTs//9.3e-87:408.96//Hs.164042:H12594
 35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259.61//Hs.76460:U49082
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328.81//Hs.89887:D38081
 R-NT2RP2003108//ESTs//2.3e-82:398.98//Hs.5105:AA115512
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336.86//Hs.101996:AB002345
 40 R-NT2RP2003121//ESTs//2.0e-75:380.96//Hs.133127:AA133355
 R-NT2RP2003125
 R-NT2RP2003129//EST//0.68:115.69//Hs.122196:AA780986
 R-NT2RP2003137//ESTs//2.1e-37:259.85//Hs.63169:N78506
 R-NT2RP2003161//ESTs//2.5e-88:451.96//Hs.29041:W37379
 R-NT2RP2003164//ESTs//4.3e-113:543.97//Hs.8980:AA629067
 45 R-NT2RP2003165//ESTs//6.9e-83:486.89//Hs.138632:H97952
 R-NT2RP2003177//ESTs//0.47:38.100//Hs.61790:AA421156
 R-NT2RP2003194//ESTs//4.7e-118:582.96//Hs.27266:AA053816
 R-NT2RP2003206//ESTs//0.032:388.58//Hs.122148:AA442074
 R-NT2RP2003230//ESTs//8.8e-103:478.99//Hs.40140:AI079253
 50 R-NT2RP2003237//ESTs//2.7e-76:392.96//Hs.106278:R37661
 R-NT2RP2003243//ESTs//3.6e-53:300.92//Rs.18793:AA192438
 R-NT2RP2003265//ESTs. Highly similar to protein NGD5 [M.musculus]//3.3e-110:557.96//Hs.24994:AA236937
 R-NT2RP2003272//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228.89//Hs.107201:W52859
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565.95//Hs.154919:AB014525
 55 R-NT2RP2003280//ESTs//2.6e-101:541.94//Hs.6982:AA622427
 R-NT2RP2003286//ESTs//1.2e-104:497.98//Hs.113052:AI222106
 R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458.74//Hs.154326:D42087

R-NT2RP2003295/Protein serine/threonine kinase sk2/0.31:321:57/Hs.1087.L20321
R-NT2RP2003297/ESTs//3.0e-15:118:87/Hs.16621:AA098874
R-NT2RP2003308/ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]/4.8e-109:553.96/Hs.26089:AA195126
R-NT2RP2003329/ESTs//0.99:208:62/Hs.143607:A1424948
R-NT2RP2003339/ESTs//1.3e-85:441:96/Hs.24115:N32618
R-NT2RP2003347/ESTs//1.5e-70:365.96/Hs.155773:A1312825
R-NT2RP2003367/EST//5.8e-80:376:100/Hs.112500:AA599014
R-NT2RP2003391/ESTs//2.8e-98:484:97/Hs.5842:AA534476
R-NT2RP2003393/ESTs//2.0e-96:510:93/Hs.75844:AA115502
R-NT2RP2003394/EST//5.2e-06:264:63/Hs.144234:W52249
R-NT2RP2003401/ESTs//6.1e-25:161:90/Hs.155360:AA984683
R-NT2RP2003433/ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/1.2e-106:508:98/Hs.131840:A1016073
R-NT2RP2003445/ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/5.6e-21:161:70/Hs.43153:N22360
R-NT2RP2003446/ESTs, Weakly similar to C27H6.4 [C.elegans]/6.0e-105:529.96/Hs.8055:W60903
R-NT2RP2003456/EST//7.5e-96:449.99/Hs.25362:A1277332
R-NT2RP2003480/ESTs//1.6e-116:583.96/Hs.59757:AA176121
R-NT2RP2003499/ESTs, Weakly similar to elastin like protein [D.melanogaster]/7.0e-71:365.95/Hs.101056:R52777
R-NT2RP2003506/ESTs, Weakly similar to ORF YPL207 [S.cerevisiae]/12.3e-115:577.96/Hs.16277:N36831
R-NT2RP2003511/ESTs//1.6e-22:182.85/Hs.28249:AA203733
R-NT2RP2003513/Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566.94/Hs.78482:Y16270
R-NT2RP2003517/Platelet-derived growth factor beta polypeptide (simian sarcoma virus (v-sis) oncogene homolog)/4.9e-62:518:79/Hs.1976:M12783
R-NT2RP2003522/ESTs//2.0e-97:462.99/Hs.24512:D60170
R-NT2RP2003533/ESTs//4.4e-45:273.78/Hs.144225:AA704101
R-NT2RP2003543/EST//1.0:80:68/Hs.65646:F13684
R-NT2RP2003559/ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.8e-58:316.94/Hs.28891:W72439
R-NT2RP2003564/ESTs//3.2e-112:528.99/Hs.53940:N46696
R-NT2RP2003581/ESTs//1.3e-88:506.93/Hs.16157:AA203719
R-NT2RP2003596/ESTs, Weakly similar to No definition line found [C.elegans]/4.7e-101:495.98/Hs.34627:AA126463
R-NT2RP2003604/Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501.97/Hs.58488:U97067
R-NT2RP2003629/EST//0.032:440:59/Hs.135297:A1038981
R-NT2RP2003643/ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [E.coli]/9.1e-62:359.92/Hs.12492:AA203188
R-NT2RP2003668/EST//9.4e-110:535.97/Hs.116279:AA628951
R-NT2RP2003687/EST//5.9e-05:196.65/Hs.139064:AA135523
R-NT2RP2003691/ESTs, Weakly similar to F59C6.9 [C.elegans]/1.0:202:62/Hs.65539:A148540
R-NT2RP2003702/ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]/4.3e-99:492.96/Hs.93332:AA811920
R-NT2RP2003704/ESTs//1.0:155:63/Hs.104166:AA740246
R-NT2RP2003706/Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265.93/Hs.78494:AB011097
R-NT2RP2003713/EST//0.81:210:59/Hs.14551:T79401
R-NT2RP2003714/ESTs//1.7e-99:495.96/Hs.158101:A1365003
R-ntntntntntntntntnt/Human 19.8 kDa protein mRNA, complete cds//0.84:221:60/Hs.2384:U18914
R-NT2RP2003737/ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]/2.4e-50:302.90/Hs.19196:W74577
R-NT2RP2003751
R-NT2RP2003760/ESTs//2.6e-101:548.93/Hs.115987:AA483808
R-NT2RP2003764/ESTs//8.2e-25:134.98/Hs.64036:AA127709
R-NT2RP2003769/ESTs//1.7e-108:545.95/Hs.56847:AA541606
R-NT2RP2003770/Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531.96/Hs.90436:AF047437

R-NT2RP2003777//ESTs//2.6e-59:323.94//Hs.10101:AI381811
 R-NT2RP2003781//ESTs//2.0e-25:269.75//Hs.144951:N34836
 R-NT2RP2003793//ESTs//8.7e-94:466.97//Hs.93949:AA782955
 R-NT2RP2003840//ESTs//3.4e-97:533.93//Hs.16130:AA195077
 5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351.65//Hs.75196:X69838
 R-NT2RP2003859//ESTs//3.0e-07:96.81//Hs.153262:AA551124
 R-NT2RP2003871//ESTs//1.9e-102:509.97//Hs.25726:AA430167
 R-NT2RP2003885//ESTs//1.0e-102:502.97//Hs.36353:AA702341
 R-NT2RP2003912//EST//1.2e-38:336.76//Hs.134975:AI094611
 10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190.60//Hs.75875:U49278
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568.97//Hs.35086:AB014458
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540.97//Hs.7302:AB007916
 15 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568.96//Hs.7316:AB018347
 R-NT2RP2003984
 R-NT2RP2003986//ESTs//4.9e-36:272.82//Hs.158268:AA738087
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519.99//Hs.36093:AI149968
 20 R-NT2RP2004014//ESTs//8.4e-102:483.99//Hs.22867:AI417478
 R-NT2RP2004041
 R-NT2RP2004042//ESTs//1.5e-105:466.97//Hs.7296:N29706
 R-ntnnnnnnnnnnnn//ESTs//1.4e-110:559.96//Hs.71916:AA219699
 25 R-NT2RP2004081//ESTs//3.7e-105:503.98//Hs.27542:AA977204
 R-NT2RP2004098//EST//7.3e-26:203.87//Hs.21897:R41461
 R-NT2RP2004124//ESTs//1.1e-83:435.95//Hs.43299:N23036
 R-NT2RP2004142//EST//1.3e-06:165.65//Hs.146742:AI147500
 R-NT2RP2004152//ESTs//7.0e-98:455.100//Hs.17731:AI342241
 30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthracidaris crassispina]//1.0e-118:583.97//Hs.16520:AI224533
 R-NT2RP2004170//ESTs//6.7e-66:407.88//Hs.157138:AI348544
 R-NT2RP2004172//ESTs//1.5e-109:567.95//Hs.159091:AA033974
 R-NT2RP2004187//ESTs//3.6e-92:488.93//Hs.22954:W26589
 35 R-NT2RP2004194//ESTs//6.2e-114:585.95//Hs.18778:AA203167
 R-NT2RP2004196
 R-NT2RP2004207//ESTs//6.3e-102:488.98//Hs.22878:AA604756
 R-NT2RP2004226//ESTs//8.8e-18:252.71//Hs.11924:W26972
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499.98//Hs.143460:AA483305
 40 R-NT2RP2004239//ESTs//1.2e-16:171.80//Hs.16134:AA203116
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530.93//Hs.54900:AF039687
 R-NT2RP2004242//ESTs//1.3e-85:460.93//Hs.104535:AA211483
 45 R-NT2RP2004245//ESTs//6.4e-117:575.97//Hs.23744:AA035744
 R-NT2RP2004270//ESTs//1.0:95.69//Hs.141371:H92187
 R-NT2RP2004300//ESTs//4.4e-80:379.99//Hs.130874:AA905056
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544.96//Hs.61152:AF000416
 50 R-NT2RP2004321//ESTs//2.1e-18:104.99//Hs.107207:AA044788
 R-NT2RP2004339//EST//1.4e-47:309.86//Hs.161917:AA483223
 R-NT2RP2004347
 R-NT2RP2004364//ESTs//1.1e-113:566.96//Hs.25880:AI268173
 R-NT2RP2004365//ESTs//0.022:271.62//Hs.38897:AI129310
 55 R-NT2RP2004366//ESTs//9.5e-71:335.100//Hs.91867:AI218624
 R-NT2RP2004373//ESTs//4.2e-25:172.87//Hs.83243:N32192
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:108.82//Hs.30490:AA146916

R-NT2RP2004392//ESTs//3.4e-81:427.94//Hs.5827:AA581646
 R-NT2RP2004396//EST//5.6e-06:100.77//Hs.138623:H92473
 R-NT2RP2004399//EST//0.98:337.59//Hs.118446:N67900
 R-NT2RP2004400//ESTs//2.1e-90:422.100//Hs.152460:AA602921
 5 R-NT2RP2004412//ESTs//1.4e-105:503.98//Hs.15929:AA403121
 R-NT2RP2004425//EST//0.00017:225.60//Hs.146935:AI168124
 R-NT2RP2004476//ESTs//1.4e-88:477.94//Hs.4859:N29695
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//
 8.6e-34:143.98//Hs.154729:AF017995
 10 R-NT2RP2004512//ESTs//2.6e-91:426.100//Hs.94133:AI270700
 R-NT2RP2004523//ESTs//1.6e-74:377.97//Hs.14217:R61320
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279.89//Hs.89887:D38081
 R-NT2RP2004551//ESTs//0.47:147.66//Hs.131519:AI024347
 R-NT2RP2004568//ESTs//1.3e-107:567.94//Hs.65234:AA195470
 15 R-NT2RP2004580//ESTs//5.9e-29:156.98//Hs.147801:AI221661
 R-NT2RP2004587//ESTs//1.0e-102:495.97//Hs.91662:AA781126
 R-NT2RP2004594//ESTs//4.1e-56:298.95//Hs.24641:AA954666
 R-NT2RP2004600//ESTs//4.8e-67:374.93//Hs.49762:N69862
 R-NT2RP2004602//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:
 20 149.76//Hs.12845:N28835
 R-NT2RP2004614//ESTs//1.0e-111:557.96//Hs.37892:N53497
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587.96//Hs.5198:AJ006291
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520.96//Hs.29956:
 AB007929
 25 R-NT2RP2004675//ESTs//2.7e-82:407.97//Hs.116113:F18930
 R-NT2RP2004681//NUCLEOLIN//0.34:387.58//Hs.79110:M60858
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600.96//Hs.154919:
 AB014525
 R-NT2RP2004709//ESTs//1.1e-106:511.98//Hs.38034:AI149793
 30 R-NT2RP2004710//ESTs//9.9e-87:477.93//Hs.6834:AA203433
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594.96//Hs.4236:
 AB007947
 R-NT2RP2004743//ESTs//2.1e-48:327.88//Hs.43635:AA447015
 R-NT2RP2004767//EST//4.0e-57:328.81//Hs.142796:N51423
 35 R-NT2RP2004775//ESTs//9.4e-60:326.94//Hs.115339:AA136774
 R-NT2RP2004791//ESTs//3.2e-82:367.96//Hs.141911:N64013
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
 8.0e-116:564.96//Hs.40820:AF058953
 R-NT2RP2004802//ESTs//6.5e-111:586.94//Hs.90375:W74579
 40 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584.97//Hs.67052:
 AF054179
 R-NT2RP2004841//EST//3.8e-31:323.74//Hs.147714:AI219906
 R-NT2RP2004861//EST//0.92:147.63//Hs.23064:R20803
 R-NT2RP2004897//ESTs//1.7e-46:390.80//Hs.139225:H96567
 45 R-NT2RP2004936//EST//0.97:176.63//Hs.137436:AA280529
 R-nnnnnnnnnnn//ESTs//0.059:137.64//Hs.144109:AI345543
 R-NT2RP2004961//ESTs//1.8e-87:409.100//Hs.138297:AA781941
 R-NT2RP2004962//ESTs//0.0021:292.59//Hs.145917:AI275458
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506.75//Hs.154326:D42087
 50 R-NT2RP2004978//ESTs//0.95:138.63//Hs.13619:W93496
 R-NT2RP2004982//ESTs//7.8e-95:468.97//Hs.22545:R43910
 R-NT2RP2004985
 R-NT2RP2004999//ESTs//2.9e-94:450.98//Hs.128766:AI149902
 R-NT2RP2005000
 55 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577.95//Hs.155972:
 AB014515
 R-NT2RP2005003//EST//1.3e-75:387.96//Hs.140843:R42235
 R-nnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568.97//Hs.31575:AF100141

- R-NT2RP2005018//ESTs//7.5e-46:280.90//Hs.126857:AA932161
 R-NT2RP2005020//ESTs//1.6e-105:554.94//Hs.14846:AA148507
 R-NT2RP2005031//EST//3.1e-79:379.99//Hs.139709:AA227887
 R-NT2RP2005037//ESTs//5.3e-102:551.93//Hs.26516:AA195220
 R-NT2RP2005038//ESTs//5.8e-101:566.92//Hs.46964:N49757
 R-NT2RP2005108
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518.97//Hs.22616:AB014564
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464.85//Hs.100555:X98743
 R-NT2RP2005139//ESTs//1.0e-108:545.95//Hs.21006:AA523383
 R-NT2RP2005140//ESTs//4.3e-90:422.99//Hs.62180:AI341261
 R-NT2RP2005144//ESTs//0.91:162.62//Hs.52399:AI075744
 R-NT2RP2005147//ESTs//4.6e-100:502.96//Hs.27931:AA633438
 R-NT2RP2005159//ESTs//7.5e-105:533.95//Hs.109819:AI357582
 R-NT2RP2005162//ESTs//6.6e-83:419.96//Hs.113998:HS0648
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513.95//Hs.155218:AJ007509
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577.96//Hs.7600:H98166
 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359.82//Hs.154103:AF061258
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245.97//Hs.21090:AA418587
 R-NT2RP2005254//ESTs//3.3e-111:581.94//Hs.22549:AA524503
 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412.95//Hs.23047:N66596
 R-NT2RP2005276//ESTs//4.6e-85:426.96//Hs.24550:AA316272
 R-NT2RP2005287//ESTs//1.7e-109:565.94//Hs.81976:AI279001
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594.98//Hs.27007:AF060219
 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545.96//Hs.44766:AJ007590
 R-NT2RP2005293//ESTs//5.1e-116:538.99//Hs.62180:AI341261
 R-NT2RP2005315//ESTs//1.4e-82:415.97//Hs.155829:AA018338
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272.91//Hs.1569:U11701
 R-NT2RP2005336//ESTs//1.9e-93:444.99//Hs.110966:AA151699
 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445
 R-NT2RP2005354//ESTs//7.2e-22:148.91//Hs.153783:H14544
 R-NT2RP2005360//ESTs//0.048:225.60//Hs.7602:AA099247
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248.82//Hs.93121:AB018304
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461.88//Hs.70849:AA121697
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491.95//Hs.7194:AI185631
 R-NT2RP2005441//ESTs//1.1e-110:548.96//Hs.5209:AA780068
 R-NT2RP2005453//ESTs//0.94:352.58//Hs.25870:H14423
 R-NT2RP2005457//ESTs//2.1e-46:236.97//Hs.19522:AA975096
 R-NT2RP2005464//ESTs//1.8e-72:349.99//Hs.44045:N51307
 R-NT2RP2005465//ESTs//0.0058:322.58//Hs.127009:AI378936
 R-NT2RP2005472//ESTs//0.47:309.60//Hs.144838:AI222019
 R-NT2RP2005476//ESTs//5.1e-40:205.9811//Hs.101577:AI168526
 R-NT2RP2005490//ESTs//L.3e-70:364.96//Hs.134382:AA083573
 R-NT2RP2005491//EST//0.012:220.60//Hs.144448:AA812455
 R-NT2RP2005495//ESTs//1.2e-86:501.91//Hs.99445:R93540
 R-NT2RP2005496//ESTs//3.2e-34:263.81//Hs.70279:AA757426
 R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284.88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84.404.98//Hs.143812:AI141755
 R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME
 I [Schizosaccharomyces pombe]//8.2e-36.215.92//Hs.5298:AA725071
 5 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:
 570:9411Hs.119023:AF092563
 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:
 433.95//Hs.36942:AA524535
 R-NT2RP2005531//EST//0.98e-64.70//Hs.146573:AI139856
 10 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108.560.94//Hs.159597:
 AJ012449
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115.583.96//Hs.62515:
 AB007963
 R-NT2RP2005549//EST//0.61:111.62//Hs.147482:AI215572
 R-NT2RP2005555//ESTs//6.6e-108.507.99//Hs.68613:AI357567
 15 R-NT2RP2005557//ESTs//3.1e-105.495.99//Hs.105985:AA885169
 R-NT2RP2005581//ESTs//1.7e-79.445.92//Hs.138152:H03240
 R-NT2RP2005600//ESTs//1.3e-38.192.100//Hs.48329:W92733
 R-NT2RP2005605//ESTs//7.6e-87.409.99//Hs.45005:AA975060
 R-NT2RP2005620//ESTs//2.9e-96.463.97//Hs.7407:AI376788
 20 R-NT2RP2005622//ESTs//1.8e-104.497.98//Hs.22595:AA394229
 R-NT2RP2005637//EST//2.5e-20.163.71//Hs.161164:AI418211
 R-NT2RP2005640//ESTs//5.0e-99.473.98//Hs.23467:AA708740
 R-NT2RP2005645//ESTs//9.5e-23.231.77//Hs.5534:AA195173
 R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103.525.96//Hs.70589:
 25 AA868470
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223.60//Hs.162:X16302
 R-NT2RP2005699//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14.87.100//Hs.146406:AF069987
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91.434.98//
 Hs.25664:AF089814
 30 R-NT2RP2005683//ESTs//1.5e-98.494.96//Hs.22595:AA394229
 R-NT2RP2005690//ESTs//4.8e-43.286.86//Hs.150727:AI292236
 R-NT2RP2005694//EST//3.1e-82.386.100//Hs.149391:AI273643
 R-NT2RP2005701//ESTs, Highly similar to BUTYROPOLIN PRECURSOR [Bos taurus]//2.8e-68:376.93//Hs.
 9095:AA532630
 35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105.503.98//Hs.61638:
 AB018342
 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105.500.98//
 Hs.14298:AI417523
 R-NT2RP2005722//EST//6.5e-76.395.94//Hs.142150:AA223982
 40 R-NT2RP2005723//ESTs//1.5e-84.452.93//Hs.91753:R44455
 R-NT2RP2005726//ESTs//3.5e-64.500.82//Hs.100526:AI223153
 R-NT2RP2005741//ESTs//4.7e-60.333.93//Hs.107242:R40258
 R-NT2RP2005748//ESTs//3.4e-102.498.97//Hs.82660:N78064
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42.223.96//
 45 Hs.159651:AF068868
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104.494.98//Hs.
 26285:AF082516
 R-NT2RP2005763//ESTs//1.1e-97.456.99//Hs.65412:AI362163
 R-NT2RP2005767//ESTs//8.0e-38.204.96//Hs.18460:AA193463
 50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-
 112.559.96//Hs.14214:AI189379
 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108.544.96//Hs.
 22151:AI214321
 R-NT2RP2005781//ESTs//1.7e-43.217.99//Hs.144391:AA365664
 55 R-NT2RP2005784//EST//0.0071:217.60//Hs.117332:AA699724
 R-NT2RP2005804//ESTs//8.8e-107.512.98//Hs.15496:W44398
 R-NT2RP2005812//ESTs//9.0e-76.359.99//Hs.113937:AI298746
 R-NT2RP2005815//ESTs//5.5e-76.363.99//Hs.136230:AA594981

- R-NT2RP2005835//ESTs//1.5e-100:541.94//Hs.86813:N25122
 R-NT2RP2005841//ESTs//2.8e-105:556.92//Hs.69993:AA628403
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
 R-NT2RP2005857//ESTs//1.0e-115:576.96//Hs.30663:AI338462
 5 R-NT2RP2005859//ESTs//7.3e-116:571.97//Hs.85986:AA195105
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
 R-NT2RP2005890//ESTs//1.0e-96:466.98//Hs.122579:AA766315
 R-NT2RP2005901//ESTs//8.3e-116:548.98//Hs.66296:AI125268
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:
 10 94//Hs.16667:T92427
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
 R-NT2RP2005942//ESTs//5.6e-117:582.96//Hs.146123:AI338419
 R-NT2RP2005980//ESTs//6.9e-101:478.98//Hs.43145:AA776988
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398.80//Hs.113283:AF018080
 15 R-NT2RP2006038//ESTs/0.025:284:59//Hs.97852:AA404347
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II
 [C.elegans]//1.2e-50:278.94//Hs.7194:AI185631
 R-NT2RP2006052//ESTs//5.0e-52:272.95//Hs.99545:AA461492
 R-NT2RP2006069//ESTs//1.8e-90:495.93//Hs.43654:AA522714
 20 R-NT2RP2006071//ESTs//1.5e-38:218.94//Hs.107882:W72093
 R-NT2RP2006098//ESTs//2.9e-105:540.95//Hs.26860:N56918
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254.62//
 Hs.46440:U21943
 R-NT2RP2006103//ESTs//1.5e-86:416.98//Hs.152114:AA401365
 25 R-NT2RP2006141//ESTs//5.3e-88:432.98//Hs.77480:AA100522
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255.72//Hs.154103:AF061258
 R-NT2RP2006184//ESTs//8.4e-101:487.98//Hs.58009:W69435
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553.95//Hs.109299:
 AB014554
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U97276
 R-NT2RP2006200//ESTs//6.5e-77:398.96//Hs.163953:R01398
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532.90//Hs.153910:X96484
 R-NT2RP2006237//ESTs//1.2e-57:305.95//Hs.86149:AI341312
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183.91//Hs.4048:AA404253
 35 R-NT2RP2006259//ESTs//3.2e-87:462.94//Hs.141556:N49928
 R-NT2RP2006261//ESTs//3.4e-57:326.92//Hs.22523:W02999
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481.97//Hs.3404:AF035262
 R-NT2RP2006320//EST//3.4e-21:335.65//Hs.141603:N66015
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460.96//Hs.21889:
 40 N78664
 R-NT2RP2006323//ESTs//3.5e-91:439.98//Hs.61697:AI081771
 R-NT2RP2006333//ESTs//4.9e-38:301.82//Hs.155999:AA196412
 R-NT2RP2006334//EST//3.1e-45:264.91//Hs.149599:AI282321
 R-NT2RP2006365//ESTs//2.9e-81:417.95//Hs.11814:W44411
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:
 77//Hs.1361:M55053
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155.76//Hs.
 115325:DB4488
 R-NT2RP2006441//ESTs//6.0e-108:529.97//Hs.101282:N45092
 50 R-NT2RP2006454//ESTs//9.2e-20:110.99//Hs.144687:AI341146
 R-NT2RP2006456//ESTs//7.1e-91:508.92//Hs.12488:W63595
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524.97//Hs.72160:AJ006266
 R-NT2RP2006467//EST//0.9e-140:61//Hs.146958:AI174478
 R-NT2RP2006472//ESTs//3.3e-92:473.95//Hs.29216:AA916679
 55 R-NT2RP2006534//ESTs//1.2e-83:394.99//Hs.162116:AA524947
 R-NT2RP2006554//ESTs//1.0e-87:460.95//Hs.47095:AA181474
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886
 R-NT2RP2006571//ESTs//2.6e-56:306.94//Hs.98370:AA316622

- R-nnnnnnnnnnn/ESTs//2.0e-112:533:98//Hs.18685:AI393829
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112
 R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598
 5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219
 R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213
 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202
 10 R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095
 R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574
 R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241
 15 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418
 R-NT2RP3000186
 20 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306
 R-NT2RP3000233//EST//1.7e-77:368:99//Hs.49075:N64817
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
 25 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
 R-NT2RP3000251
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
 30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
 R-NT2RP3000324
 35 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177
 R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
 40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185
 45 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
 R-NT2RP3000433
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
 50 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408
 R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600
 55 R-NT2RP3000487//ESTs//0.012:384:60//Hs.86684:AA885141
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
 R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

- R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]/0.95:85.71//Hs.5184:AA079151
 R-NT2RP3000542//ESTs/2.6e-53:375.84//Hs.44158:N30180
 R-NT2RP3000561//EST//1.1e-13:170.75//Hs.148421:AI198036
 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071
 R-NT2RP3000578//ESTs/2.6e-68:324:100//Hs.5445:AA779447
 R-NT2RP3000582//ESTs/2.1e-25:131:80//Hs.152465:AA563785
 R-NT2RP3000584//ESTs/1.8e-97:460.99//Hs.120698:AI241511
 R-NT2RP3000590//ESTs/2.0e-97:453:100//Hs.105355:AA953817
 R-NT2RP3000592//ESTs/2.8e-91:432:99//Hs.144304:AI190916
 R-NT2RP3000599//ESTs/3.8e-93:437.99//Hs.23971:AA829880
 R-NT2RP3000605//ESTs/4.2e-111:554:96//Hs.40780:AA422049
 R-NT2RP3000622//ESTs/2.0e-100:473:99//Hs.11387:AI127394
 R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]/5.4e-115:545:98//Hs.4857:AI090739
 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315
 R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]/6.3e-92:434:99//Hs.152517:AA719022
 R-NT2RP3000644//ESTs/1.0e-44:306.84//Hs.155498:W27084
 R-NT2RP3000661//ESTs/3.1e-95:470.97//Hs.126069:W76185
 R-NT2RP3000665//ESTs/3.3e-95:503.94//Hs.34313:W81185
 R-NT2RP3000685//ESTs/2.7e-99:515.94//Hs.9711:R60873
 R-NT2RP3000690//ESTs/3.3e-88:414.99//Hs.1465:89:AI085578
 R-NT2RP3000736
 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-ESTERASE DELTA 1 [Rattus norvegicus]/1.8e-07:114:75//Hs.136065:W21960
 R-NT2RP3000753//ESTs/3.1e-99:461:100//Hs.150901:AI310447
 R-NT2RP3000759//ESTs/2.0e-74:384.95//Hs.104222:AA207243
 R-NT2RP3000815//ESTs/8.5e-97:455.99//Hs.158897:AI378583
 R-NT2RP3000825//EST//0.0089:343.59//Hs.42897:N20810
 R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
 R-NT2RP3000836//ESTs/6.8e-24:181.84//Hs.134464:AI151081
 R-NT2RP3000841//ESTs/4.5e-93:491.93//Hs.23618:H98082
 R-NT2RP3000845//ESTs/2.4e-88:473.93//Hs.8312:AA813022
 R-NT2RP3000847//ESTs/9.3e-89:460.95//Hs.154106:AI051657
 R-NT2RP3000850
 R-NT2RP3000852//Fibrillin 2//0.55:237.63//Hs.79432:U03272
 R-NT2RP3000859//ESTs/1.4e-96:509.94//Hs.7187:AA576895
 R-NT2RP3000865//EST//4.8e-23:461.66//Hs.162088:AA505741
 R-NT2RP3000868//ESTs/5.4e-78:430.93//Hs.102796:N70837
 R-NT2RP3000869//ESTs/8.5e-77:397.94//Hs.84848:AI014673
 R-NT2RP3000875//Mevalonate kinase//3.8e-78:531.84//Hs.75138:M88468
 R-NT2RP3000901//ESTs/2.1e-95:466.97//Hs.10647:AA428217
 R-NT2RP3000904//ESTs/1.6e-79:380.99//Hs.100850:AA479385
 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]/9.5e-113:566:96//Hs.5900:AA035728
 R-NT2RP3000919
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407
 R-NT2RP3000980//ESTs/3.3e-72:364.96//Hs.9536:AA114178
 R-NT2RP3000994//ESTs/3.5e-111:537.97//Hs.21146:AA683542
 R-NT2RP3001004//ESTs/9.6e-91:456.96//Hs.58974:W87405
 R-NT2RP3001007//ESTs/6.7e-99:482.97//Hs.117737:AI088029
 R-NT2RP3001055//ESTs/0.0012:294.60//Hs.66479:AA863044
 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]/5.6e-102:486.99//Hs.145956:AA007349
 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)/0.0012:447:58//Hs.2133:U18991
 R-NT2RP3001084//ESTs/4.3e-102:528.96//Hs.25277:W87874
 R-NT2RP3001096//ESTs/1.1e-110:540.96//Hs.42824:AA873182

- R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832
 R-nnnnnnnnnnn/DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325
 R-NT2RP300111//ESTs. Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796: C06063
- 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166
- 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305
 R-NT2RP3001147//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //9.6e-113:552:97//Hs.23900:U82984
- 15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963
- 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196
 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399
 R-NT2RP3001236//ESTs. Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
 R-NT2RP3001239//ESTs. Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048: AA524416
- 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965
- 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:U25651
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989
- 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534: U35234
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586: AB007920
 R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
- 40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
 R-NT2RP3001383//ESTs//3.6e-100:118:78//Hs.111055:AA169778
 R-NT2RP3001384//ESTs. Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90// Hs.96200:AA218942
- 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898
- 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692
 R-nnnnnnnnnnn/Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374
- 55 R-NT2RP3001447//ESTs. Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

- R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658
 R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280
 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009
 R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//
 6.8e-112:549:9711Hs.28285:AF064801
 R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
 10 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
 R-NT2RP3001554//ESTs. Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:
 AA524416
 R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
 R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
 R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798
 R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598
 R-NT2RP3001629
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915889
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
 25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
 30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
 R-NT2RP3001716//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 //4.1e-80:444:91//Hs.6823:W18181
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099
 35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
 40 R-NT2RP3001764//ESTs. Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:
 N92517
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:
 AB007928
 45 R-NT2RP3001792//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292
 R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
 50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
 R-NT2RP3001926//ESTs. Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:
 AI123300
 55 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
 R-NT2RP3001938//ESTs. Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
 //1.3e-95:483:96//Hs.5771:W74591

- R-NT2RP3001943//ESTs//1.2e-23:169.88//Hs. 103930:AA160990
 R-NT2RP3001944//ESTs//2.0e-90:439.97//Hs. 103380:AI291325
 R-NT2RP3001969//ESTs//0.95:133.65//Hs. 131669:AI025889
 R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310.99//Hs. 11449:AI021540
 5 R-NT2RP3002002//ESTs//2.1e-95:562.89//Hs. 5997:AA897088
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335.82//Hs. 75087:X86779
 R-NT2RP3002007//ESTs//0.12:184.66//Hs. 94030:AA846729
 R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291.89//Hs. 155464:AF088219
 R-NT2RP3002033
 10 R-NT2RP3002045//ESTs//1.0e-92:555.88//Hs. 106411:W29081
 R-NT2RP3002054//EST//0.45:155.63//Hs. 5656:D20426
 R-NT2RP3002056//ESTs//1.4e.95:504.93//Hs. 17428:AI365221
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127.66//Hs. 90438:D63486
 R-NT2RP3002062
 15 R-ntnnnnnnnnnn//ESTs//2.1e-113:552.97//Hs. 9591:AA069657
 R-NT2RP3002081//ESTs//5.5e-43:212.100//Hs. 124852:AA969139
 R-NT2RP3002097//EST//2.3e-10:80.91//Hs. 102717:N59148
 R-NT2RP3002102
 R-NT2RP3002108
 20 R-NT2RP3002146//ESTs//5.5e-58:296.97//Hs. 65328:AA625385
 R-NT2RP3002147//EST//2.5e-53:387.81//Hs. 147928:M249703
 R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534.96//Hs. 59523:AA602837
 R-NT2RP3002163//ESTs//2.7e-106:520.97//Hs. 21258:AA412293
 25 R-NT2RP3002165//ESTs//7.4e-93:479.95//Hs. 27299:AI074024
 R-NT2RP3002166//ESTs//1.0:261.59//Hs. 132817:AA593713
 R-NT2RP3002173//ESTs//2.7e-93:512.92//Hs. 23648:H07120
 R-NT2RP3002181//ESTs//1.0e-84:435.96//Hs. 47378:AI193598
 R-NT2RP3002244//ESTs//2.7e-11:97.89//Hs. 9412:W72446
 30 R-NT2RP3002248//ESTs//4.3e-90:459.95//Hs. 9848:AA130588
 R-NT2RP3002255//ESTs//1.3e-45:289.88//Hs. 9100:AA431672
 R-NT2RP3002273//ESTs//2.3e-100:489.97//Hs. 8258:AA744743
 R-NT2RP3002276//ESTs//1.2e-50:306.91//Hs. 16160:AA778171
 R-NT2RP3002303//ESTs//1.1e-67:323.99//Hs. 129761:AA836898
 35 R-NT2RP3002304//ESTs//2.8e-86:405.99//Hs. 29643:AA418500
 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens] //1.8e-19:136.87//Hs. 106928:AI041737
 R-NT2RP3002343//ESTs//1.0e-42:260.93//Hs. 7797:W25667
 R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221.64//Hs. 556:L41887
 40 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516.94//Hs. 6483:Y16355
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524.95//Hs. 12707:AB014578
 R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108.71//Hs. 28914:Y00486
 45 R-NT2RP3002501//ESTs//2.7e-96:489.95//Hs. 27335:N74185
 R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526.90//Hs. 8083:AA521436
 R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497.96//Hs. 6650:AA843246
 50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438.94//Hs. 19542:AB018272
 R-NT2RP3002549//ESTs//3.8e-98:493.96//Hs. 7358:AA191673
 R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184.63//Hs. 89230:AF031815
 R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138.78//Hs. 129883:AB007880
 55 R-NT2RP3002590//ESTs//2.9e-51:290.93//Hs. 162942:AJ243850
 R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58.100//Hs. 76691:AF070673
 R-NT2RP3002603
 R-NT2RP3002631//ESTs//4.8e-54:367.85//Hs. 13109:AA192514

- R-NT2RP3002659//ESTs//5.3e-30:229.85//Hs.152114:AA401365
 R-NT2RP3002660//ESTs//1.9e-88:452.95//Hs.120146:AA708573
 R-NT2RP3002663//EST//3.2e-89:469.95//Hs.105767:AA525172
 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [*Drosophila melanogaster*]/5.9e-109:537:97//Hs.19348:AA151678
 R-NT2RP3002682//ESTs//2.3e-98:541.91//Hs.75844:AA115502
 R-NT2RP3002687//ESTs//5.5e-103:498.97//Hs.72782:AA910871
 R-NT2RP3002688//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]/5.0e-101:524.95//Hs.32580:AI123601
 R-NT2RP3002701//EST//0.87:131.63//Hs.161916:AA483169
 R-NT2RP3002713//ESTs//4.7e-106:542.95//Hs.14479:AA160945
 R-NT2RP3002763//ESTs//1.3e-54:290.94//Hs.142031:AA809159
 R-NT2RP3002770//ESTs//0.047:275.61//Hs.122984:AA526973
 R-NT2RP3002785//ESTs//2.4e-52:255.99//Hs.132959:AI376958
 R-NT2RP3002799//EST//8.2e-61:321.94//Hs.140992:R71377
 R-NT2RP3002810//EST//0.19:116.68//Hs.121810:AA775240
 R-NT2RP3002818//ESTs//1.3e-109:531.98//Hs.58924:AI348080
 R-NT2RP3002861//ESTs//2.5e-84:429.95//Hs.23920:AA909678
 R-NT2RP3002869//EST//0.00011:116.71//Hs.161606:AA019641
 R-NT2RP3002876//ESTs//0.0024:182.63//Hs.117306:AA687262
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146.72//Hs.129727:AF035587
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570.95//Hs.6162:AB018314
 R-NT2RP3002911//ESTs//3.6e-92:436.99//Hs.143917:AI206286
 R-NT2RP3002948//EST//1.0:102.65//Hs.144730:AI191975
 R-NT2RP3002953//ESTs//1.8e-107:513.98//Hs.119693:AI201698
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563.56//Hs.127338:AB007961
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [*Saccharomyces cerevisiae*]/112.0e-56:387.86//Hs.144597:W20143
 R-NT2RP3002972//ESTs//1.7e-97:502.96//Hs.7274:AA476850
 R-NT2RP3002978//ESTs//8.6e-104:498.98//Hs.118923:AA252116
 R-NT2RP3002988//EST//1.2e-59:315.94//Hs.157743:AI360553
 R-NT2RP3003008//ESTs//1.4e-97:515.94//Hs.6544:AA524423
 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POLYPROTEIN [*Mus musculus*]/3.0e-100:528.94//Hs.90353:N98551
 R-NT2RP3003059//ESTs//1.7e-76:398.95//Hs.102971:W05355
 R-NT2RP3003061//ESTs//4.9e-82:414.96//Hs.99603:AI141912
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [*C. elegans*]/5.9e-83:392.99//Hs.101364:AA534439
 R-NT2RP3003071//ESTs//6.3e-85:399.99//Hs.109755:AA180809
 R-NT2RP3003078//ESTs//1.0e-98:471.99//Hs.7995:AI359466
 R-NT2RP3003101//EST//0.032:235.60//Hs.147920:AI202441
 R-NT2RP3003121//ESTs//3.0e-47:238.97//Hs.43559:AI003520
 R-NT2RP3003133//EST//1.5e-77:395.96//Hs.142150:AA223982
 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [*Mus musculus*]/3.3e-107:535.96//Hs.27437:AA004208
 R-NT2RP3003139//ESTs//2.5e-106:504.98//Hs.106795:AI271632
 R-NT2RP3003150//ESTs//1.6e-99:539.91//Hs.46500:AA129774
 R-NT2RP3003157//ESTs//1.5e-114:563.97//Hs.58608:AA081007
 R-NT2RP3003185//ESTs//3.9e-93:443.98//Hs.9741:AI131226
 R-NT2RP3003193//ESTs//2.0e-37:428.71//Hs.33354:AA179944
 R-NT2RP3003197//ESTs//5.8e-56:312.94//Hs.7016:AA215796
 R-NT2RP3003203//EST//0.0073:212.63//Hs.161355:AI422634
 R-NT2RP3003204//ESTs//7.4e-52:253.99//Hs.120146:AA708573
 R-NT2RP3003212//ESTs//1.8e-76:401.95//Hs.29067:N26107
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [*Dictyostelium discoideum*]/2.0e-40:229.93//Hs.17377:AI078151
 R-NT2RP3003242//ESTs//8.3e-97:458.99//Hs.23057:AI290343

- R-NT2RP3003251//ESTs//1.5e-60.320.95//Hs.36495:AA151628
 R-NT2RP3003264//ESTs//2.1e-103.521.95//Hs.4094:AA173960
 R-NT2RP3003278//ESTs//8.2e-109.536.96//Hs.23788:AA524061
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102.550.93//Hs.11702:L36983
 R-NT2RP3003290//EST//4.3e-27.372.70//Hs.159131:AI384035
 R-NT2RP3003301//ESTs//4.4e-56.285.97//Hs.95370:AA601055
 R-NT2RP3003302//EST//7.2e-10.395.63//Hs.162554:AA584818
 R-NT2RP3003311//ESTs//4.2e-110.538.97//Hs.62180:AI341261
 R-NT2RP3003313//ESTs//2.1e-106.531.96//Hs.22630:C05931
 R-NT2RP3003327//ESTs//4.3e-102.518.95//Hs.120355:AA625445
 R-NT2RP3003330//ESTs//8.6e-104.497.97//Hs.72071:AI125289
 R-NT2RP3003344//ESTs//2.5e-105.494.99//Hs.112188:AA872993
 R-NT2RP3003346//ESTs//1.0:123.69//Hs.116029:AA813102
 R-NT2RP3003353//EST//0.0014:162.68//Hs.149191:AI246155
 R-NT2RP3003377//EST//4.5e-15:119.85//Hs.148129:AA885567
 R-NT2RP3003384//EST//0.0057:86.74//Hs.127735:AA962272
 R-NT2RP3003385//ESTs//0.64:347.59//Hs.5646:W72721
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418.67//Hs.139488:AI124095
 R-NT2RP3003409//ESTs//5.3e-98:479.97//Hs.155198:AA767372
 R-NT2RP3003411//ESTs//4.8e-96:416.97//Hs.129059:AA126041
 R-NT2RP3003427//ESTs//7.4e-103.510.96//Hs.25303:AA641023
 R-NT2RP3003433//ESTs//3.5e-85.405.99//Hs.63131:AA664156
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97.479.96//Hs.14934:AF004828
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102.527.93//Hs.26450:AB018268
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106.549.94//Hs.7886:AI057529
 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401.60//Hs.75307:U02556
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(GTG)n repeat-containing mRNA//4.1e-33:217.88//Hs.8068.U00952
 R-NT2RP3003552//ESTs//3.1e-106.546.94//Hs.101754:AI123430
 R-NT2RP3003555//ESTs//3.4e-106.537.95//Hs.85550:AA187681
 R-NT2RP3003564
 R-NT2RP3003572//ESTs//1.2e-20:122.88//Hs.8253:N48721
 R-NT2RP3003576//ESTs//2.7e-71.394.94//Hs.151136:R99944
 R-NT2RP3003589//EST//0.58:242.59//Hs.130804:AA894759
 R-NT2RP3003625//ESTs//7.6e-41:349.80//Hs.140608:N53448
 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222.60//Hs.17217:U49957
 R-NT2RP3003659//ESTs//2.0e-113.547.97//Hs.23389:AA769310
 R-NT2RP3003665//ESTs//1.6e-80.415.95//Hs.141084:H11714
 R-NT2RP3003672
 R-NT2RP3003686//ESTs//6.8e-114.552.97//Hs.43299:N23036
 R-NT2RP3003701//ESTs//2.1e-16:282.66//Hs.115512:AI208768
 R-NT2RP3003716//ESTs//2.1e-45:195.91//Hs.41296:N71923
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103.492.97//Hs.48513:AB018300
 R-NT2RP3003746//ESTs//1.9e-85.411.98//Hs.54835:AI050863
 R-NT2RP3003795//EST//6.2e-97:459.99//Hs.134769:AI089747
 R-NT2RP3003799//ESTs//2.8e-62.337.94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108.551.95//Hs.115742:AF077754
 R-NT2RP3003805//ESTs//2.2e-103.490.99//Hs.9412:W72446
 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89.456.95//Hs.5555:AI285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173.89//Hs.2180:M57627
 R-NT2RP3003825//ESTs//1.6e-66.485.80//Hs.7405:W27761

- R-NT2RP3003828//ESTs, Weakly similar to unknown. [H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224
 R-NT2RP3003831//ESTs//2.2e-38:317.79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611
- 5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-NT2RP3003870//ESTs//3.4e-82:449.92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs//1.9e-89:449.96//Hs.45046:N40170
 R-NT2RP3003914//ESTs//1.3e-99:470.98//Hs.118966:AA926726
- 10 R-NT2RP3003918//ESTs//1.3e-79:417.94//Hs.5005:W25933
 R-NT2RP3003932//ESTs//6.0e-83:427.94//Hs.93581:H50221
 R-NT2RP3003989//ESTs//4.8e-76:403.93//Hs.127243:W80409
 R-NT2RP3003992//ESTs//2.4e-88:508.90//Hs.134200:D19593
 R-NT2RP3004013//ESTs//3.7e-111:551.97//Hs.105108:AA781142
- 15 R-NT2RP3004016//ESTs//1.7e-81:394.98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs//3.5e-69:386.93//Hs.51347:T72820
 R-NT2RP3004070//ESTs//5.5e-108:552.9511Hs.23392:AI310139
 R-NT2RP3004078//ESTs//3.3e-82:443.93//Hs.26407:W4537
- 20 R-NT2RP3004093//ESTs//4.4e-83:426.94//Hs.140932:AI262104
 R-NT2RP3004095//ESTs//0.00013:93.78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402.95//Hs.55847:W31092
 R-NT2RP3004125//ESTs//9.3e-74:363.97//Hs.32988:C01696
- 25 R-NT2RP3004145//ESTs//2.6e-96:451.99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs//1.3e-10:77.92//Hs.135890:AI183425
 R-NT2RP3004155//ESTs//1.7e-110:558.96//Hs.27003:AI279093
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200.100//Hs.26089:AA195126
- 30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266.89//Hs.6314:AA522619
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547.97//Hs.99819:AI346680
 R-NT2RP3004215//ESTs//1.1e-103:541.95//Hs.124918:N64794
 R-NT2RP3004242//ESTs//4.5e-105:524.96//Hs.29724:N46252
- 35 R-NT2RP3004246//EST//1.1e-07:67.91//Hs.125687:AA884827
 R-NT2RP3004253//EST//2.9e-88:454.94//Hs.127713:AA961628
 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468.95//Hs.5117:AA831530
 R-NT2RP3004262//ESTs//4.1e-86:443.96//Hs.101393:T87623
- 40 R-NT2RP3004334//EST//0.00057:206.63//Hs.149388:AI273630
 R-NT2RP3004341//EST//0.00042:151.68//Hs.148498:AI200264
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299.85//Hs.154103:AF061258
 R-NT2RP3004349//EST//3.6e-42:175.88//Hs.161917:AA483223
 R-NT2RP3004378//ESTs//0.27:294.60//Hs.66479:AA863044
- 45 R-NT2RP3004399//ESTs//5.8e-99:479.98//Hs.120234:AA732224
 R-NT2RP3004424//EST, Highly similar to F21C4.6 [C.elegans]//0.30:253.58//Hs.97184:AA385934
 R-NT2RP3004428//ESTs//2.8e-48:279.91//Hs.106826:W25985
 R-NT2RP3004451//ESTs//4.8e-101:509.96//Hs.29725:W74621
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526.98//Hs.27349:AB007917
- 50 R-NT2RP3004466//ESTs//0.25:51.90//Hs.7778:AA195616
 R-NT2RP3004470//EST//0.032:70.71//Hs.147925:AI249332
 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521.97//Hs.5003:AB007925
 R-NT2RP3004480
- 55 R-NT2RP3004490//ESTs//4.7e-68:354.95//Hs.163721:H42504
 R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508.95//Hs.47393:AA218858

R-NT2RP3004503//ESTs/4.6e-90:478.93//Hs.133998;AA994735
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]/1.8e-83:465.92//Hs.137064;AA318257
R-NT2RP3004507//ESTs/1.5e-98:495.96//Hs.128905;AI051971
R-NT2RP3004527//ESTs/1.6e-109:535.97//Hs.194981;AI279865
R-nnnnnnnnnnnn
R-NT2RP3004544//EST/0.035:226.60//Hs.99195;AA449232
R-NT2RP3004566//ESTs/4.1e-86:455.95//Hs.13110;T67461
R-NT2RP3004569//ESTs/2.9e-94:493.94//Hs.24944;AA977674
R-NT2RP3004572//ESTs/1.1e-92:437.99//Hs.24846;AI20493
R-NT2RP3004578//ESTs/0.98:166.64//Hs.124593;AA854456
R-NT2RP3004594//EST//5.8e-89:426.98//Hs.134213;AI080213
R-NT2RP3004617//ESTs/1.4e-40:226.85//Hs.15921;R71157
R-NT2RP3004618//ESTs/1.8e-38:229.90//Hs.125153;AA543723
R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds/7.2e-57:291.95//Hs.8786;AB014680
R-NT2RP4000008//ESTs/8.9e-119:561.98//Hs.25035;AI123335
R-NT2RP4000023//EST//1.2e-34:271.80//Hs.98300;AA418560
R-NT2RP4000035//Small inducible cytokine A5 (RANTES)/2.1e-68:320.82//Hs.155464;AF088219
R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289.82//Hs.51233;AF016266
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]/8.3e-98:462.97//Hs.10114;AI345945
R-NT2RP4000078//ESTs/0.00068:367.60//Hs.106090;AA547030
R-NT2RP4000102//ESTs/9.7e-50:256.97//Hs.24266;R28287
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536.96//Hs.57929;AB011538
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554.97//Hs.64691;AB007952
R-NT2RP4000147//ESTs/3.9e-11:122.80//Hs.25584;AA632014
R-NT2RP4000150//EST//4.4e-84:510.88//Hs.144238;W52294
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]/5.7e-93:515.92//Hs.8083;AA521436
R-NT2RP4000159//ESTs/0.0019:209.65//Hs.161816;AA400295
R-NT2RP4000167//ESTs/2.1e-113:549.97//Hs.109441;N66569
R-NT2RP4000185//ESTs/0.65:232.59//Hs.144445;AA807257
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505.96//Hs.13999;AB014600
R-NT2RP4000212//ESTs//8.5e-14:169.75//Hs.85392;AA081788
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272.90//Hs.40100;AB002390
R-NT2RP4000218//ESTs/6.1e-10:335.64//Hs.105658;AA978185
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354.96//Hs.155481;AJ006470
R-NT2RP4000246//ESTs//7.1e-26:154.94//Hs.14838;AA502757
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379.99//Hs.43728;AF091092
R-NT2RP4000263
R-nnnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.elegans]/4.7e-104:525.96//Hs.152069;AA548972
R-NT2RP4000312//ESTs/8.2e-66:319.99//Hs.35091;AI271631
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513.99//Hs.13410;AF070524
R-NT2RP4000323//ESTs//7.7e-109:534.97//Hs.34790;AA192760
R-NT2RP4000355//ESTs//3.1e-44:320.83//Hs.141323;N80390
R-NT2RP4000367//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520.99//Hs.107479;AB018281
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527.98//Hs.31323;AF044195
R-NT2RP4000370//ESTs//8.9e-32:166.98//Hs.70488;AI301130
R-NT2RP4000376//ESTs//6.8e-99:465.99//Hs.27182;AA604498
R-NT2RP4000381//ESTs//3.0e-50:280.93//Hs.8395;W27376
R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA vk30b3.5 [C.elegans]/3.9e-87:499

- 91//Hs.26156:AA630975
 R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTER-
 GENIC REGION [Saccharomyces cerevisiae]/8.9e-95:468:96//Hs.93871:AI191318
- 5 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011
 R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955
 R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953
 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-
 plete cds//0.35:153:63//Hs.113286:U77783
- 10 R-ntnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740
 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167
 R-ntnnnnnnnnnn
- 15 R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III
 [C.elegans]/1.2e-40:125:97//Hs.56124:AI424792
 R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713
 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868
 R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874
 R-NT2RP4000519
- 20 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.norvegicus]/3.4e-93:496:93//Hs.107394:H07126
 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213
 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]/8.2e-92:448:98//Hs.
 25597:H93026
 R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840
 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263
- 25 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531
 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393
 R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704
 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651
 R-NT2RP4000724//ESTs//1.5e-83:442:94//Hs.142114:AA205615
- 30 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399
 R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211
 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:
 AB007939
- 35 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834
 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028
 R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104
 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356
 R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185
- 40 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617
 R-ntnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594
 R-ntnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]/5.9e-17:134:85//Hs.14146:W92235
 R-ntnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683
- 45 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//
 Hs.24812:AF069532
 R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905
 R-NT2RP4000955//ESTs//3.5e-10:119:78//Hs.42946:N21111
 R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986
- 50 R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179
 R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017
 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123
 R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018
 R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620
- 55 R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-28:439:68//Hs.
 129735:AF010144
 R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769
 R-NT2RP4001006//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]/6.6e-124:574:99//Hs.

- 47393:AA218858
 R-NT2RP4001010//EST//2.8e-31:194.90//Hs.161186:AI418635
 R-NT2RP4001029//ESTs//4.4e-111:523.99//Hs.28423:AI336292
 R-NT2RP4001041//ESTs. Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]/3.6e-114:569.96//Hs.6762:AA088424
 R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282.94//Hs.100955:AB007859
 R-NT2RP4001064//ESTs. Weakly similar to protein B [H.sapiens]/2.1e-103:485.99//Hs.10114:AD45945
 R-NT2RP4001078
 R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial/1.7e-119:569.98//Hs.106778:AJ010953
 R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548.95//Hs.13273:AB011164
 R-NT2RP4001095//ESTs//1.5e-113:563.96//Hs.118732:AI344055
 R-NT2RP4001100//ESTs//2.0e-46:413.79//Hs.146314:R99617
 R-NT2RP4001117//EST//7.4e-51:294.92//Hs.7260:T23737
 R-NT2RP4001122//ESTs//5.4e-109:509.99//Hs.16390:AI052357
 R-NT2RP4001126//EST//0.97:169.61//Hs.148107:AA693476
 R-NT2RP4001138//ESTs//3.0e-110:543.97//Hs.57655:AI056890
 R-NT2RP4001143//ESTs. Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]/5.4e-113:573.96//Hs.5249:U55977
 R-NT2RP4001148//ESTs//3.1e-103:490.98//Hs.121282:AI091453
 R-NT2RP4001149//EST//1.7e-50:281.93//Hs.101727:H16171
 R-NT2RP4001150//ESTs//1.9e-90:422.100//Hs.125490:AI138884
 R-NT2RP4001159
 R-NT2RP4001174//ESTs//2.5e-110:526.98//Hs.116555:AA639278
 R-nnnnnnnnnnnnn//ESTs//1.1e-25:140.97//Hs.83756:AI002822
 R-NT2RP4001207//ESTs//4.4e-70:432.89//Hs.13109:AA192514
 R-NT2RP4001210//ESTs//1.4e-108:509.99//Hs.27021:AI359495
 R-NT2RP4001213//ESTs. Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]/4.4e-123:624.95//Hs.22744:AI379892
 R-NT2RP4001219//ESTs//0.0043:142.65//Hs.6733:AI160750
 R-NT2RP4001228//ESTs//4.9e-101:482.98//Hs.62684:AA806103
 R-NT2RP4001235//ESTs//3.7e-105:571.93//Hs.37706:AA005120
 R-NT2RP4001256//ESTs//1.1e-12:189.74//Hs.20621:W28255
 R-NT2RP4001260//EST//6.9e-05:313.61//Hs.116438:AA648430
 R-NT2RP4001274//EST//0.0020:246.63//Hs.149955:AI289933
 R-nnnnnnnnnnnnn//ESTs//2.9e-34:213.91//Hs.43100:AA186588
 R-NT2RP4001313
 R-NT2RP4001315//EST//6.1e-38:217.93//Hs.97832:AA400892
 R-NT2RP4001339//ESTs//3.8e-91:430.99//Hs.34840:AI279612
 R-NT2RP4001345//ESTs//5.3e-89:443.96//Hs.6770:AA92732
 R-NT2RP4001351//ESTs//6.0e-78:394.97//Hs.102796:N70837
 R-NT2RP4001353//ESTs//4.8e-06:90.82//Hs.7778:AA195616
 R-NT2RP4001372
 R-NT2RP4001373//ESTs. Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]/1.7e-108:546.96//Hs.32271:AA203680
 R-NT2RP4001375//ESTs//2.4e-19:155.87//Hs.62119:AA043299
 R-NT2RP4001379//EST//4.4e-29:288.72//Hs.157848:AI362501
 R-NT2RP4001389//ESTs. Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]/3.8e-79:438.93//Hs.21938:W81045
 R-NT2RP4001407//ESTs//8.3e-112:541.97//Hs.22587:AA743132
 R-NT2RP4001414//ESTs//8.6e-18:117.90//Hs.90789:W27649
 R-NT2RP4001433//ESTs. Moderately similar to PROHIBITIN [H.sapiens]/1.6e-102:498.97//Hs.62386:AA512948
 R-NT2RP4001442//ESTs//8.8e-104:489.99//Hs.101619:AI339433
 R-NT2RP4001447
 R-NT2RP4001474
 R-NT2RP4001483//ESTs//2.1e-100:528.92//Hs.17860:AA706655
 R-NT2RP4001498//ESTs//1.1e-97:470.98//Hs.95744:AI392846

- R-NT2RP4001502//ESTs//6.7e-73.382.96//Hs.11874:N93511
 R-NT2RP4001507//ESTs//2.6e-57.302.96//Hs.65328:AA625385
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107.546.96//Hs.5570:AI377863
 R-NT2RP4001529//ESTs//3.3e-112.524.99//Hs.28423:AI336292
 5 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Parametium tetraurelia]//2.8e-120.566.98//Hs.108530:AA523928
 R-nnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26.184:88//Hs.136189:AA133224
 R-NT2RP4001555//ESTs//1.1e-95.445.100//Hs.134403:AA677552
 10 R-NT2RP4001567//ESTs//2.8e-106.506.98//Hs.102708:AA292285
 R-NT2RP4001568//ESTs//6.4e-55.300.94//Hs.57442:N63437
 R-NT2RP4001571//ESTs//1.3e-114.556.97//Hs.30340:AA521251
 R-NT2RP4001574//ESTs//0.0035.120.67//Hs.96339:AA225906
 R-NT2RP4001575
 15 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]//8.7e-112.557.97//Hs.7558:AA526812
 R-NT2RP4001610//ESTs//6.2e-77.382.96//Hs.21543:AA166776
 R-NT2RP4001614//ESTs//2.8e-117.565.98//Hs.9591:AA069657
 R-NT2RP4001634//ESTs//2.0e-39.213.96//Hs.32360:AA534737
 20 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116.559.97//Hs.5332:AF007151
 R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36.192.97//Hs.5662:AA868361
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104.525.96//Hs.20472:W28734
 25 R-NT2RP4001677//ESTs//1.8e-105.522.97//Hs.106390:AA156805
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118.583.96//Hs.15562:U96629
 R-NT2RP4001725//ESTs//2.0e-11.141.74//Hs.117589:N25941
 R-nnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-CURSOR [D.melanogaster]//3.4e-73.362.97//Hs.152332:AI141922
 30 R-NT2RP4001739//ESTs//6.6e-59.340.91//Hs.122293:AA843692
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113.552.96//Hs.2481:X78926
 R-NT2RP4001760//ESTs//2.5e-94.453.98//Hs.122579:AA766315
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62.326.94//Hs.110839:W28098
 35 R-NT2RP4001803
 R-NT2RP4001822//ESTs//4.4e-98.526.92//Hs.96908:AI161133
 R-NT2RP4001823//ESTs//1.7e-72.357.97//Hs.144900:AI218434
 R-NT2RP4001828//ESTs//3.3e-101.536.92//Hs.18851:AA857826
 40 R-NT2RP4001838//ESTs//4.2e-58.344.90//Hs.48723:N66663
 R-NT2RP4001849//EST//0.24.105.71//Hs.136747:AA749210
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34.212.88//Hs.154326:D42087
 R-NT2RP4001893//ESTs//3.0e-58.321.95//Hs.158787:W79602
 R-NT2RP4001896//EST//3.8e-15.108.92//Hs.160835:AI345528
 45 R-NT2RP4001901//ESTs//1.2e-110.536.97//Hs.31443:AI018606
 R-NT2RP4001927//ESTs//2.1e-105.546.93//Hs.73291:AI417099
 R-NT2RP4001938//ESTs//2.8e-40.235.78//Hs.163641:R61848
 R-NT2RP4001946//ESTs//1.3e-29.175.93//Hs.43703:AA088436
 R-NT2RP4001950//ESTs//4.6e-95.458.98//Hs.150890:AI341793
 50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)/2.3e-62.310.82//Hs.73919:X81637
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87.457.94//Hs.41793:AA775879
 R-NT2RP4001975//ESTs//1.9e-52.281.94//Hs.7704:W58252
 R-NT2RP4002018
 55 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09.90.86//Hs.41127:AA555184
 R-NT2RP4002052//ESTs//0.054.353.60//Hs.117510:AA903738
 R-NT2RP4002058//EST//7.8e-26.151.94//Hs.124617:AA855106

R-NT2RP4002071//ESTs/6.9e-98:475.92//Hs.49216:AA916679
R-NT2RP4002075//ESTs/0.67:121.65//Hs.153939:AI284198
R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464.82//Hs.144228:N99507
R-NNNNNNNNNN//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271.100//Hs.6185:AA428565
R-NT2RP4002083//ESTs/2.0e-108:548.96//Hs.6120:W80407
R-NT2RP4002408//ESTs/2.6e-77:391.96//Hs.14014:AA745592
R-NT2RP4002791//ESTs/7.9e-101:527.93//Hs.22394:NC2555
R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373.92//Hs.31532:H18272
R-NT2RP4002905//ESTs/1.5e-107:517.98//Hs.40460:N36090
R-ABOVAC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605.94//Hs.108258:AB007934
R-OVARC1000004
R-OVARC1000006//ESTs/1.5e-19:139.89//Hs.143034:AI26929
R-OVARC1000013//ESTs/5.9e-98:531.93//Hs.16470:AA121635
R-OVARC1000014//ESTs/0.24:243.60//Hs.19569:AA464273
R-OVARC1000017
R-OVARC1000035//ESTs/0.035:252.63//Hs.134123:AI078286
R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331.83//Hs.96247:X95073
R-OVARC1000060//EST//2.8e-28:348.71//Hs.141728:W73041
R-OVARC1000068//ESTs/3.0e-83:491.90//Hs.29397:NI5367
R-OVARC1000071//ESTs/2.5e-60:321.96//Us.25010:R6787
R-OVARC1000085//Proteasome component C5//8.6e-67:366.92//Hs.75748:AL031259
R-NNNNNNNNNN//ESTs/1.0e-111:526.98//Hs.129020:AI380703
R-OVARC1000091//ESTs, Highly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596.94//Hs.20597:W58370
R-OVARC1000092//ESTs/5.1e-18:144.82//Hs.109140:AI289942
R-OVARC1000106
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495.97//Hs.3688:AF069250
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489.74//Hs.101238:Y11312
R-OVARC1000133//EST//0.00028:284.61//Hs.30547:H05482
R-OVARC1000145//EST//3.9e-40:201.99//Hs.156148:AI2333214
R-OVARC1000148//EST//0.79:150.62//Hs.100078:T05090
R-OVARC1000151
R-OVARC1000168//EST//1.7e-19:142.90//Hs.38441:H66023
R-OVARC1000191//EST//0.0072:292.63//Hs.132492:AA922629
R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339.81//Hs.154103:AF061258
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196.92//Hs.64322:AA142864
R-OVARC1000212//EST//0.20:178.61//Hs.133031:AI049874
R-OVARC1000240//ESTs/9.0e-64:314.98//Hs.42300:AA204958
R-OVARC1000241//EST//0.00018:115.68//Hs.150728:AI123130
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.7e-74:403.93//Hs.108117:AI097079
R-OVARC1000302//EST//4.0e-14:102.90//Hs.136617:AA630476
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191.98//Hs.20725:AI027777
R-OVARC1000309//ESTs/3.6e-66:348.94//Hs.9547:AA532449
R-OVARC1000321//ESTs/3.6e-87:454.95//Hs.110445:AA044743
R-OVARC1000328//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488.96//Hs.125749:AI377682
R-OVARC1000335//ESTs/3.0e-115:565.97//Hs.54835:AI050863
R-OVARC1000347//EST//0.0018:145.65//Hs.136945:AA765672
R-OVARC1000384//ESTs/2.8e-38:253.89//Hs.15093:AA203423
R-OVARC1000408//ESTs/2.6e-98:515.94//Hs.119808:C05928

R-*OVARC*1000411//ESTs//3.2e-82;395.98/Hs.104747:AA406219
R-*OVARC*1000414//Landsteiner-Wienner blood group glycoprotein//1.5e-27;211.79/Hs.108287:L27670
R-*OVARC*1000042//ESTs//2.8e-38;255.74/Hs.138525:R99237
R-*OVARC*1000427//EST//2.6e-58;302.96/Hs.122914:AA767034
5 R-*OVARC*1000431//ESTs//4.9e-108;551.96/Hs.11668:A123426
R-*OVARC*1000437
R-*OVARC*1000440//ESTs//2.9e-91;456.96/Hs.93701:A1018671
R-*OVARC*1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45;320.84/Hs.73614:U83460
10 R-*OVARC*1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79;418.94/Hs.12334:AB014583
R-*OVARC*1000461//ESTs//3.1e-62;342.93/Hs.23241:R46582
R-*OVARC*1000465//ESTs//1.7e-67;349.95/Hs.127238:AA477576
R-*OVARC*1000466//ESTs//1.9e-66;337.95/Hs.5212:A421211
15 R-*OVARC*1000473//ESTs//5.4e-89;320.99/Hs.29173:AA134926
R-*OVARC*1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102;514.96/Hs.11833:A1299947
R-*OVARC*1000486//ESTs//3.9e-78;405.95/Hs.98312:AA424983
R-*OVARC*10000496
R-*OVARC*1000520//ESTs//1.2e-20;145.88/Hs.87456:AA434484
20 R-*OVARC*1000526//Small inducible cytokine A5 (RANTES)//8.9e-47;217.87/Hs.155464:AF088219
R-*OVARC*1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48;264.92/Hs.49860:AA702248
R-*OVARC*1000543//ESTs//5.7e-74;410.94/Hs.62817:AA047021
R-*OVARC*1000556//Hs.sapiens mRNA for ribosomal S6 kinase//9.5e-27;202.85/Hs.90859:X85106
R-*OVARC*1000557//EST//2.8e-18;169.79/Hs.149101:A1244285
25 R-*OVARC*1000564//EST//2.3e-34;199.92/Hs.146637:A141587
R-*OVARC*1000573//Interleukin 10//4.7e-42;300.83/Hs.2180:M57627
R-*OVARC*1000578//Small inducible cytokine A5 (RANTES)//5.2e-58;392.84/Hs.155464:AF088219
R-*OVARC*1000588//EST//1.8e-41;174.85/Hs.163333:AA879053
R-*OVARC*1000605
30 R-*OVARC*100622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47;417.77/Hs.159897:AB007970
R-*OVARC*1000640//H.sapiens mRNA for translin associated protein X//1.9e-28;366.72/Hs.96247:X95073
R-*OVARC*1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31;162;100/Hs.111862:AB011162
35 R-*OVARC*1000678//EST//0.92;199.60/Hs.122025:AA778480
R-nnnnnnnnnnnn//ESTs//0.94;416.59/Hs.130754:AA279522
R-*OVARC*1000681//EST//9.2e-21;179.80/Hs.132635:A1032875
R-*OVARC*1000689//Homo sapiens ataxin-7 (SCAT7) mRNA, complete cds//0.053;160.64/Hs.108447-AJ000517
R-*OVARC*1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09;141.73/Hs.32511:AB007901
40 R-*OVARC*1000703//ESTs//1.7e-46;298.87/Hs.138856:H47461
R-*OVARC*1000730//ESTs, Weakly similar to C2F2F2 gene product [C.elegans]//1.7e-17;137.86/Hs.7049:A114736
R-*OVARC*1000746//ESTs//0.16;366.60/Hs.136969:AA830918
R-*OVARC*1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-28;430.69/Hs.42457:AA523306
45 R-*OVARC*1000771//ESTs//1.3e-87;461.94/Hs.22399:AA531016
R-*OVARC*1000781//ESTs//8.3e-119;572.97/Hs.41972:AA626793
R-*OVARC*1000787//ESTs//7.4e-18;115.93/Hs.164036:AA845659
R-*OVARC*1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19;119.95/Hs.3069:L11066
50 R-*OVARC*1000802//ESTs//2.2e-41;383.78.Hs.161228:A149764
R-*OVARC*1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106;536.95/Hs.61628:Y17711
R-*OVARC*1000846//Clathrin, light polypeptide (Lcbj)/1.6e-66;282.87/Hs.73919:X81637
R-*OVARC*1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115;579.96/Hs.18910:AF045584
55 R-*OVARC*1000862//EST//4.3e-14;129.81/Hs.150663:AA923096
R-*OVARC*1000876//ESTs//1.0e-115;573.96/Hs.87287:A150674
R-*OVARC*1000883//ESTs//3.5e-109;523.98/Hs.28423:A1336292
R-*OVARC*1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENE

REGION [Bacillus subtilis]/7.9e-98:525:93//Hs.10366:W21953
 R-OVARC1000886//ESTs/8.2e-79:417:94//Hs.7729:AA830777
 R-OVARC1000891//ESTs/6.8e-75:401:94//Hs.5833:H15401
 R-OVARC1000897//ESTs/3.5e-91:440:98//Hs.125264:AA873350
 5 R-OVARC1000912
 R-OVARC1000915//ESTs/1.0e-45:328:82//Hs.163980:AA715814
 R-OVARC1000924//ESTs/1.0e-100:501:96//Hs.30204:AA497127
 R-OVARC1000936//EST/3.0e-74:367:98//Hs.145098:AA421696
 R-OVARC1000937//EST/1.1e-53:290:95//Hs.162846:AA631215
 10 R-OVARC1000945//ESTs/4.9e-51:301:89//Hs.20100:W25794
 R-OVARC1000948//ESTs/3.7e-67:332:98//Hs.112570:AA621971
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)/7.2e-44:283:86//Hs.155464:AF088219
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
 R-OVARC1000971//EST/6.2e-05:126:70//Hs.160491:AL254909
 15 R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.elegans]/3.5e-68:346:96//Hs.25544:AA532784
 R-OVARC1000996//EST/0.12:92:71//Hs.117141:AA678811
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
 R-OVARC1001000//ESTs/1.8e-22:198:80//Hs.140608:N53448
 20 R-OVARC1001004//Human kpnI repeat mna (cdna clone pcd-kpnI-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
 R-OVARC1001010//EST/2.1e-09:92:85//Hs.147893:AI223270
 R-OVARC1001011//EST/2.4e-14:200:75//Hs.149290:AI248117
 R-OVARC1001032//EST/2.7e-29:304:73//Hs.141733:W80630
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:
 25 137:74//Hs.77579:AF013263
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
 R-OVARC1001040//ESTs/2.9e-87:415:99//Hs.132812:AI032046
 R-OVARC1001044//ESTs/1.1e-83:432:96//Hs.55043:N94384
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
 30 R-OVARC1001055//ESTs/2.4e-23:238:76//Hs.141421:H99231
 R-OVARC1001062//ESTs/3.4e-92:469:96//Hs.34658:N98652
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:
 AF082657
 R-OVARC1001072//ESTs/1.3e-34:227:89//Hs.126704:W95844
 35 R-OVARC1001074
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,
 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds//3.3e-75:366:95//Hs.26584:
 40 AF051782
 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.
 46468:U45984
 R-OVARC1001118//ESTs/5.3e-99:485:97//Hs.130815:AA936548
 R-OVARC1001129//ESTs/9.8e-66:351:95//Hs.18616:T99312
 45 R-OVARC1001161//ESTs, Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]/2.2e-
 66:346:95//Hs.53263:AA173226
 R-OVARC1001162//EST/1.5e-44:376:80//Hs.161917:AA483223
 R-OVARC1001167//ESTs/4.7e-110:548:96//Hs.35254:AI133727
 R-OVARC1001169//ESTs/0.22:152:68//Hs.149424:AI274200
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)/1.8e-42:305:84//Hs.155464:AF088219
 R-OVARC1001173//EST/2.5e-35:182:84//Hs.161917:AA483223
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:
 80//Hs.97203:U83171
 R-OVARC1001188//ESTs/4.1e-18:296:69//Hs.139197:AA228343
 55 R-OVARC1001200//ESTs/2.0e-28:207:85//Hs.35121:AA877826
 R-OVARC1001232//ESTs/3.2e-61:358:91//Hs.6449:W95025
 R-OVARC1001240//ESTs/6.7e-45:316:85//Hs.121675:AA629668
 R-OVARC1001243//ESTs/2.3e-86:409:99//Hs.163091:AA742361

- R-OVARC1001261//ESTs//0.63:125.64//Hs.155743:AI344166
 R-OVARC1001268//ESTs//8.1e-20:113.98//Hs.109477:AA477929
 R-OVARC1001270//ESTs//1.5e-107:530.97//Hs.62905:AA460708
 R-OVARC1001271//ESTs//4.5e-36:401.72//Hs.20190:AA525532
 5 R-OVARC1001282//EST//4.0e-91:428.99//Hs.145599:AI263113
 R-OVARC1001296//ESTs//2.6e-63:301.100//Hs.125753:AA740885
 R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334.100//Hs.23763:AB011090
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304.83//Hs.73919:X81637
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147.63//Hs.76494:U41344
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452.76//Hs.155464:AF088219
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464.93//Hs.23651:AA650356
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568.95//Hs.118690:X67247
 15 R-OVARC1001344//EST//3.6e-44:341.81//Hs.162197:AA535216
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250.93//Hs.3337:M90657
 R-OVARC1001360//ESTs//5.2e-110:534.98//Hs.24743:AA843844
 R-OVARC1001369//ESTs//1.7e-98:478.97//Hs.7729:AA830777
 R-OVARC1001372//ESTs//2.6e-97:456.99//Hs.153648:AI341415
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344.72//Hs.153468:AB011147
 R-OVARC1001381//ESTs//5.1e-19:200.66//Hs.114031:AA700958
 R-OVARC1001391
 R-nnnnnnnnnnn//ESTs//0.003 9:48.95//Hs.117964:N20913
 25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561.95//Hs.21586:AB006651
 R-OVARC1001419
 R-OVARC1001425//EST//5.7e-20:395.66//Hs.159707:AI393136
 R-OVARC1001436//ESTs//9.6e-90:427.99//Hs.6982:AA622427
 R-OVARC1001442//ESTs//1.1e-66:317.100//Hs.18437:AI206345
 30 R-OVARC1001453//ESTs//2.0e-20:163.84//Hs.133503:AA628592
 R-OVARC1001476//EST//0.23:125.66//Hs.71444:AA131700
 R-OVARC1001480//ESTs//3.1e-56:181.97//Hs.40109:AA928694
 R-OVARC1001489//ESTs//1.0:297.58//Hs.86723:AA393089
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585.96//Hs.6534:AF016507
 35 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283.90//Hs.155464:AF088219
 R-OVARC1001525//EST//0.80:170.60//Hs.157398:AI364539
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566.95//Hs.6396:AB016492
 R-OVARC1001547//ESTs//5.7e-105:564.93//Hs.68835:AA088388
 40 R-OVARC1001577//Homo sapiens SRP46 splicing factor retrospseudogene mRNA//4.4e-20:150.89//Hs.155160:AF031166
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282.72//Hs.154326:D42087
 R-OVARC1001610//ESTs//4.6e-108:555.95//Hs.44295:N32019
 R-OVARC1001611//ESTs//0.0021:117.71//Hs.135568:AA972965
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114.78//Hs.5158:AB007869
 R-OVARC1001668//ESTs//1.0:127.69//Hs.153290:AI022659
 R-OVARC1001702//ESTs//4.8e-44:225.97//Hs.96855:AA346854
 R-OVARC1001703//ESTs//2.3e-89:426.99//Hs.27099:W60080
 R-OVARC1001711//ESTs//1.9e-57:251.99//Hs.9732:AA527784
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236.81//Hs.15485:AA046954
 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422.90//Hs.102824:X05276
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300.83//Hs.144563:AF057280
 55 R-nnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:540.92//Hs.117741:AA903456
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567.94//Hs.155377:U97670

R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575

R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127

R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604

5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978

R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333

R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688

R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831

10 R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110

R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621

R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160

R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809

15 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:AF070611

R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476

R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147

20 R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

25 R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892

30 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531

35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934

R-OVARC1002068//ESTs//8.5e-97:455:99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315

40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860

R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691

45 R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825

R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.122957:AA478923

R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631

R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160

R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478

50 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337

R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557

R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223

55 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870

R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440

R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503

R-PLACE10000501//ESTs//9.7e-90:453:96//Hs.27410:N25612

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

- egans]/[3.9e-40:224.94//Hs.87889:AA262008
 R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence/[6.5e-27:531.66//Hs.133342:AF070536
 R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds/[8.5e-103:513.96//Hs.31921:AB014548
- 5 R-PLACE1000786//ESTs/[5.2e-93:449.97//Hs.58389:W74482
 R-NNNNNNNNNN/H.sapiens mRNA for chemokine HCC-1/[0.88:201.60//Hs.20144:AF088219
 R-PLACE1000798//ESTs/[1.1e-97:508.94//Hs.139119:N32189
 R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]/[7.7e-31:220.86//Hs.117576:R33135
- 10 R-NNNNNNNNNN/ESTs/[1.8e-87:459.94//Hs.43100:AA186588
 R-PLACE1000856//ESTs/[0.0084:224.59//Hs.145906:AI275039
 R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]/[2.2e-92:467.95//Hs.6118-AI141558
 R-PLACE1000909//ESTs/[4.7e-89:435.97//Hs.95744:AI392846
- 15 R-PLACE1000931//EST/[1.9e-28:261.73//Hs.135545:AI097091
 R-PLACE1000948//ESTs/[0.034:329.58//Hs.114851:AA608697
 R-PLACE1000972//EST/[3.3e-24:264.74//Hs.130321:AI002941
 R-PLACE1000977//EST/[0.085:153.65//Hs.131646:AI025689
 R-PLACE1000979
- 20 R-PLACE1001000//ESTs/[4.7e-56:284.96//Hs.117978:AA810725
 R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]/[5.2e-63:343.93//Hs.5662:AA868361
 R-PLACE1001010//EST/[0.96:53.71//Hs.96973:AA351146
 R-PLACE1001015//Oxytocin receptor/[2.8e-25:308.71//Hs.2820:X64878
- 25 R-PLACE1001024//ESTs/[5.0e-12:79.96//Hs.97910:AA404736
 R-PLACE1001036//ESTs/[4.0e-15:301.65//Hs.137947:AI025762
 R-PLACE1001062//ESTs/[5.2e-15:199.73//Hs.138982:AA056120
 R-PLACE1001076//ESTs/[3.9e-84:406.98//Hs.115455:AA678124
 R-PLACE1001088//ESTs/[3.0e-106:518.97//Hs.158964:AA639580
- 30 R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds/[0.035:259.59//Hs.31575:AF100141
 R-PLACE1001104//ESTs/[6.1e-115:582.95//Hs.10972:AA164268
 R-PLACE1001118//ESTs/[6.9e-81:440.93//Hs.5383:AA913610
 R-PLACE1001136//ESTs/[7.4e-41:168.83//Hs.95115:AA206594
- 35 R-PLACE1001168//ESTs/[3.9e-21:116.99//Hs.5897:AA148834
 R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]/[0.91:77.71//Hs.115211:AA287527
 R-PLACE1001185//ESTs/[1.5e-65:330.96//Hs.26368:AA789297
 R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]/[1.9e-99:512.94//Hs.24884:AA176812
- 40 R-PLACE1001241//ESTs/[1.1e-81:446.93//Hs.42278:AI073464
 R-PLACE1001257//EST/[6.4e-46:298.87//Hs.162404:AA573131
 R-PLACE1001272//ESTs/[0.31:158.61//Hs.42960:N95371
 R-PLACE1001279//ESTs/[1.8e-77:376.97//Hs.29276:AA427780
- 45 R-PLACE1001280//ESTs/[1.1e-30:134.89//Hs.163492:AI334460
 R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]/[2.7e-22:181.84//Hs.48320:AA149548
 R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]/[4.2e-34:195.92//Hs.86276:W27601
- 50 R-PLACE1001311//ESTs/[9.1e-91:438.97//Hs.41055:AI339056
 R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds/[5.5e-44:215.86//Hs.50984:U01160
 R-PLACE1001351//ESTs/[2.4e-101:494.97//Hs.23944:AI097077
- 55 R-PLACE1001366//Small inducible cytokine A5 (RANTES)/[8.7e-43:284.85//Hs.155464:AF088219
 R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds/[2.3e-81:431.93//Hs.152005:AF009615
 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/[1.0e-36:192.97//Hs.12342:AF055030
- R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds/[1.0e-86:456.94//Hs.21301:AF093419
 R-PLACE1001387//ESTs/[6.0e-74:383.94//Hs.55016:AI298280

- R-PLACE1001395//ESTs//2.3e-94.473.95//Hs.22394:N32555
 R-PLACE1001399//ESTs//2.6e-41.204.100//Hs.24462:N36348
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45.242.95//Hs.110404:AF091087
- 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
 R-PLACE1001440
 R-PLACE1001456//EST//0.76:120.62//Hs.34011:H48115.
 R-PLACE1001468//ESTs//4.0e-80.403.96//Hs.131832:AI017547
 R-PLACE1001484//ESTs//3.0e-16.201.72//Hs.153413:AJ248625
- 10 R-PLACE1001502//ESTs//8.1e-31:161.99//Hs.126264:AA455617
 R-PLACE1001503//ESTs//2.4e-37:176.81//Hs.141581:AA315361
 R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339.90//Hs.4742:AB006969
 R-PLACE1001534//ESTs//3.6e-61:304.97//Hs.45207:AI042153
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170.85//Hs.155456:AA707265
- 15 R-PLACE1001551//ESTs//1.5e-39:202.98//Hs.139269:AA894431
 R-PLACE1001570//EST//1.1e-70:495.82//Hs.144234:W52249
 R-PLACE1001602//EST//0.33:297.57//Hs.149839:AI287601
 R-PLACE1001603//ESTs//2.0e-17:181.76//Hs.155334:AA827904
- 20 R-PLACE1001610//EST//1.1e-86:442.95//Hs.112580:AA608683
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217.97//Hs.75258:AF054174
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458.91//Hs.114547:AA167095
- 25 R-PLACE1001634//ESTs//0.0035:40.97//Hs.101577:AI168526
 R-PLACE1001640//ESTs//0.0028:377.57//Hs.131044:D61640
 R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141.62//Hs.153060:AA195804
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545.97//Hs.3688:AF069250
- 30 R-PLACE1001692//EST//3.0e-43:430.75//Hs.162975:AA679124
 R-PLACE1001705//ESTs//3.0e-81:418.94//Hs.22646:AI374903
 R-PLACE1001716//EST//0.76:150.62//Hs.128906:AA983667
 R-PLACE1001720//ESTs//2.4e-64:385.90//Hs.60455:AA010993
- 35 R-PLACE1001729//ESTs//2.9e-84:418.96//Hs.134740:AA282171
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206.89//Hs.6366:AA614113
 R-PLACE1001740//EST//6.5e-05:113.68//Hs.139949:AA644266
 R-PLACE1001745//ESTs//3.3e-92:473.95//Hs.104270:AA236479
 R-PLACE1001746//ESTs//8.8e-93:443.98//Hs.112198:AI423937
- 40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540.89//Hs.4812:AF061243
 R-PLACE1001756//ESTs//0.17:157.66//Hs.141565:N64662
 R-PLACE1001761
 R-PLACE1001771//ESTs//0.92:165.62//Hs.473.87:N51980
- 45 R-PLACE1001781//ESTs//5.7e-84:437.95//Hs.23363:AA081236
 R-PLACE1001799//EST//0.00039:126.65//Hs.123267:AA807352
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463.95//Hs.40820:AF058953
 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328.75//Hs.155464:AF088219
- 50 R-PLACE1001845
 R-PLACE1001869//EST//1.0:207.62//Hs.137298:W32868
 R-PLACE1001897//ESTs//2.4e-23:219.80//Hs.7503:H50009
 R-PLACE1001912//ESTs//1.5e-32:162.78//Hs.136810:AA789098
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363.97//Hs.17839:AF099936
- 55 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130.66//Hs.151406:AB014523
 R-PLACE1001983//ESTs//2.8e-66:334.96//Hs.110155:AA007313

- R-PLACE1001989//ESTs//1.3e-88:453.95//Hs.132717:AA171941
R-PLACE1002046
R-PLACE1002052//ESTs//1.7e-79:428.94//Hs.6737:N32595
R-PLACE1002066//ESTs//2.8e-82:427.94//Hs.132972:AA543094
5 R-PLACE1002072//ESTs//0.27:108.66//Hs.123163:AA809619
R-PLACE1002073//EST//5.5e-70:369.95//Hs.132339:AI028552
R-PLACE1002090//ESTs//6.3e-73:361.96//Hs.134469:AA731632
R-PLACE1002115//ESTs//4.6e-34:233.88//Hs.163443:R23311
10 R-PLACE1002119//ESTs//1.2e-88:444.96//Hs.15725:AA521293
R-PLACE1002140//ESTs//6.6e-22:118.100//Hs.22793:W91937
R-PLACE1002150//ESTs//4.0e-96:465.98//Hs.7312:AI167614
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400.76//Hs.162172:AA534189
15 R-PLACE1002163//ESTs//3.2e-83:428.95//Hs.137011:AI185965
R-PLACE1002171//ESTs//5.3e-68:392.90//Hs.62273:AA143745
R-PLACE1002205//ESTs//1.5e-39:211.95//Hs.26338:N48793
R-PLACE1002213//ESTs//5.1e-38:290.83//Hs.146811:AA410788
R-PLACE1002227//EST//1.3e-14:214.72//Hs.46979:N49892
R-PLACE1002256//ESTs//2.4e-100:484.98//Hs.9343:AI004257
20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501.81//Hs.23094:M19503
R-PLACE1002319//ESTs//1.4e-28:17.82//Hs.7353:AA209308
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501.93//Hs.18277:AB018271
R-PLACE1002395//ESTs//3.6e-25:248.77//Hs.3853:AA034291
R-PLACE1002399//ESTs//1.5e-27:238.78//Hs.13014:W26381
25 R-PLACE1002433//ESTs//4.3e-108:511.98//Hs.98324:AA621959
R-PLACE1002437//EST//1.2e-06:158.61//Hs.159833:T24110
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176.60//Hs.83715:X69804
R-PLACE1002450//ESTs//1.5e-89:432.98//Hs.47371:AA136333
R-PLACE1002465//ESTs//1.6e-92:488.93//Hs.78110:AA741320
30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166.85//Hs.19368:U69263
R-PLACE1002477//ESTs//2.5e-62:305.98//Hs.88605:AA421132
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307.91//Hs.17200:AF042273
R-PLACE1002499//ESTs//7.4e-72:373.96//Hs.128221:AA972429
35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296.83//Hs.5158:AB007869
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217.69//Hs.152230:AI140609
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582.85//Hs.88756:AB018256
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116.93//Hs.99348:AC004774
40 R-PLACE1002537//ESTs//4.8e-93:440.99//Hs.164005:AA766491
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555.95//Hs.23259:AA532437
R-PLACE1002578//EST//1.9e-40:337.81//Hs.162404:AA573131
R-PLACE1002583//EST//1.2e-07:264.65//Hs.156414:AI339738
45 R-PLACE1002591//ESTs//2.3e-67:372.94//Hs.143046:N73778
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228.97//Hs.7527:AA843208
R-PLACE1002604//ESTs//3.3e-106:532.96//Hs.86828:AA632147
R-PLACE1002625//EST//3.8e-13:173.74//Hs.138597:H77749
50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189.58//Hs.75703:J04130
R-PLACE1002665//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390.97//Hs.124903:AF068180
R-PLACE1002714//ESTs//8.2e-63:340.93//Hs.7973:H19830
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445.90//Hs.29202:R71586
55 R-PLACE1002768//ESTs//1.2e-70:359.95//Hs.132600:H12865
R-PLACE1002772//ESTs//8.1e-49:362.82//Hs.141254:AI334099
R-PLACE1002782//ESTs//2.4e-58:284.98//Hs.143545:AI149014

- R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
 R-PLACE1002962
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
 R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178
 25 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
 R-PLACE1003176
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
 35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326
 40 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765
 45 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
 55 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//ESTs//1.0:162:63//Hs.147003:AI184671
 R-PLACE1003493//ESTs//1.2e-73:383.95//Hs.28852:R64270
 R-PLACE1003516//ESTs//3.2e-23:206.80//Hs.138632:H97952
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236.79//Hs.2853:Z29505
 5 R-PLACE1003521//ESTs//5.8e-74:371.96//Hs.30818:AA194980
 R-PLACE1003528//ESTs//1.1e-40:219.82//Hs.138856:H47461
 R-PLACE1003537//ESTs, Weakly similar to multispinning membrane protein [H.sapiens]//7.4e-69:338.98//Hs.110439:N93209
 R-PLACE1003553//ESTs//2.2e-87:438.97//Hs.132022:AJ040321
 10 R-PLACE1003566//ESTs//1.2e-62:298.92//Hs.30799:AI052591
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145.80//Hs.92381:AB007956
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264.65//Hs.158253:R86178
 15 R-PLACE1003584
 R-PLACE1003592//ESTs//1.3e-15:213.69//Hs.139507:T77542
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459.89//Hs.23884:AD77106
 R-PLACE1003596//ESTs//0.011:273.61//Hs.71719:AA142875
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576.88//Hs.56851:D83200
 20 R-PLACE1003605//ESTs//3.7e-86:407.99//Hs.136057:AA988299
 R-nnnnnnnnnnn//ESTs//1.0:78.71//Hs.101248:T26446
 R-PLACE1003618//ESTs//6.8e-30:281.79//Hs.114455:AA411943
 R-PLACE1003625//ESTs//7.2e-78:377.98//Hs.102708:AA292285
 R-PLACE1003638//ESTs//6.7e-38:274.82//Hs.138852:AA284247
 25 R-PLACE1003669//ESTs//9.7e-83:418.95//Hs.4842:AI342607
 R-PLACE1003704//ESTs//3.0e-13:99.89//Hs.81648:W26521
 R-PLACE1003709//ESTs//0.019:178.60//Hs.32100:N59866
 R-PLACE1003711//ESTs//0.99:126.63//Hs.47005:N98639
 R-PLACE1003723//ESTs//1.7e-89:448.96//Hs.157222:AA766987
 30 R-PLACE1003738//ESTs//2.5e-36:182.100//Hs.122162:AI057087
 R-PLACE1003760//Human globin gene//L9e-98:538.91//Hs.100090:M69023
 R-PLACE1003762//EST//2.9e-15:125.85//Hs.162083:AA487512
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300.69//Hs.158302:U88965
 R-PLACE1003771//ESTs//1.2e-09:64.100//Hs.23799:AI003798
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199.97//Hs.115197:AA215757
 R-PLACE1003784//ESTs//3.7e-87:428.97//Hs.157985:AI366909
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236.88//Hs.153468:AB011147
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313.96//Hs.121020:AA526092
 40 R-PLACE1003850//ESTs//4.0e-67:351.96//Hs.159303:T91059
 R-PLACE1003858//ESTs//0.96:87.66//Hs.107112:AA679058
 R-nnnnnnnnnnn
 R-PLACE1003870//EST//2.9e-34:281.79//Hs.160895:AI365871
 45 R-nnnnnnnnnnn
 R-PLACE1003886//ESTs//6.7e-85:410.97//Hs.25129:W93595
 R-PLACE1003888//ESTs//0.0085:165.64//Hs.96739:AA441915
 R-PLACE1003900//EST//2.4e-05:129.69//Hs.127931:AA969259
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282.96//Hs.58553:AA100804
 50 R-PLACE1003915//EST//0.87:55.76//Hs.145930:AI275760
 R-PLACE1003923//ESTs//1.7e-89:456.95//Hs.14125:AA156236
 R-PLACE1003932//ESTs//3.0e-50:340.84//Hs.151208:AI126110
 R-PLACE1003936//EST//1.8e-08:208.65//Hs.162656:AA603567
 55 R-PLACE1003968//ESTs//7.4e-49:301.90//Hs.93850:AA115330
 R-PLACE1004104//ESTs//1.9e-46:254.94//Hs.96802:AA443231
 R-PLACE1004114//ESTs//1.2e-64:322.97//Hs.28928:AI052052
 R-PLACE1004118//ESTs//1.0e-83:404.98//Hs.112764:AA609770

R-PLACE1004128//ESTs//5.3e-80.415.95//Hs.11835:AA040244
 R-PLACE1004149//ESTs//7.2e-25.331.72//Hs.141084:H11714
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56.491.76//Hs.113283:AF018080
 R-PLACE1004161//ESTs//2.0e-59.355.88//Hs.13830:AA918601
 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11)mRNA, complete cds//
 4.7e-78.434.91//Hs.153504:AF044321
 R-PLACE1004197
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//
 1.5e-105.501.98//Hs.24640:AF069493
 10 R-PLACE1004242//ESTs//1.0e-71.364.87//Hs.138632:H97952
 R-PLACE1004256//EST//0.0011.347.61//Hs.131385:AI022630
 R-PLACE1004257//EST//0.027.99.71//Hs.97587:AA398209
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL, 14//0.72:180.63//Hs.117729:100124
 R-PLACE1004270//ESTs//0.011.264.59//Hs.110044:AA181800
 15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:
 121.66//Hs.1938:S82362
 R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//1.4e-107.581:
 91//Hs.127007:AF084830
 R-PLACE1004284//ESTs//5.0e-22.187.82//Hs.23141:W92114
 20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:
 279.77//Hs.39687:AA744496
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61.313.95//Hs.
 71435:AI253099
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115.590.94//Hs.11171:Y11588
 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69.572:
 77//Hs.1361:M55053
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:
 379.93//Hs.16232:AF100153
 R-PLACE1004376//ESTs//0.49.362.59//Hs.138086:AI056309
 30 R-PLACE1004384//EST//1.0.4.76//Hs.128546:AA905556
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-
 98.572.90//Hs.14202:N46000
 R-PLACE1004405//ESTs//3.4e-99.507.95//Hs.28792:AI343467
 R-PLACE1004425//ESTs//2.7e-85.442.95//Hs.12544:N53665
 35 R-PLACE1004428//ESTs//1.0e-07.114.78//Hs.140225:AA704101
 R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
 encoding mitochondrial protein, complete cds//9.4e-90.516.88//Hs.155410:U49283
 R-PLACE1004451
 R-PLACE1004460//ESTs//5.4e-14.338.64//Hs.97464:AA662980
 40 R-PLACE1004467//ESTs//3.3e-85.467.92//Hs.9527:W52721
 R-PLACE1004471//ESTs//3.0e-73.389.94//Hs.23240:R46578
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101.510.95//Hs.16986:W89194
 R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:
 278.61//Hs.89663:L13286
 45 R-PLACE1004506//ESTs//2.5e-98.559.90//Hs.19447:AI057117
 R-PLACE1004510//ESTs//1.5e-91.436.98//Hs.24846:AI420493
 R-PLACE1004516//EST//1.7e-66.344.96//Hs.99303:AA453164
 R-PLACE1004518//ESTs//5.2e-79.410.94//Hs.27091:AA436553
 R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40.332.72//Hs.
 50 115325:084488
 R-PLACE1004550
 R-PLACE1004564//ESTs//5.5e-76.367.98//Hs.49683:AA564742
 R-PLACE1004629//ESTs, Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40.272.87//Hs.7100:W07181
 R-PLACE1004645//ESTs//6.3e-14.83.100//Hs.17270:AA701903
 55 R-PLACE1004646//ESTs//3.7e-22.231.76//Hs.141250:N29734
 R-PLACE1004658//ESTs//2.0e-12.109.84//Hs.23508:AA101113
 R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23.129.99//Hs.123129:AB018257
 R-PLACE1004672//ESTs//2.0e-50.256.98//Hs.136367:AI144254

R-PLACE1004674/Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8-90.510.911/Hs.80019:AF035600

R-PLACE1004681//EST//2.1e-08:283.62//Hs.99543:AA461482

R-PLACE1004686

R-PLACE1004691//EST//7.3e-42:305.82//Hs.141833:AA021552

R-PLACE1004693/ESTs//0.014:135.64//Hs.145333:AI251374

R-PLACE1004716/ESTs, Weakly similar to No definition line found [C.elegans]/3.4e-80:413.94//Hs.23528:AI279571

R-PLACE1004722/EST//0.14:165.63//Hs.18213:T97997

R-PLACE1004736/ESTs//1.0e-72:385.94//Hs.10657:N6391

R-PLACE1004740/ESTs//1.0:267.58//Hs.101661:AA416619

R-nnnnnnnnnnnn/EST//0.45:94.69//Hs.147174:AI192195

R-PLACE1004751/EST//9.8e-32:174.83//Hs.147901:AI223374

R-PLACE1004773/Homo sapiens invasin protein mRNA, complete cds//2.7e-89:437.96//Hs.104715:AF084367

R-PLACE1004777/ESTs//7.4e-68:351.94//Hs.23395:AA398548

R-PLACE1004793/ESTs//1.3e-53:290.78//Hs.142375:AA398619

R-nnnnnnnnnnnn/Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580.88//Hs.38176:AB011178

R-PLACE1004813/ESTs//7.6e-86:433.96//Hs.85640:AA535856

R-PLACE1004814/Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358.99//Hs.3688:AF069250

R-PLACE1004815/EST//4.7e-50:333.84//Hs.142196:AA258356

R-PLACE1004824/Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450.76//Hs.73821:M35663

R-PLACE1004827/ESTs//2.3e-48:250.96//Hs.138766:AA342185

R-PLACE1004836/ESTs//2.7e-39:222.94//Hs.78661:AA195299

R-PLACE1004838/EST//0.056:198.60//Hs.129589:AA995901

R-PLACE1004840/ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381.93//Hs.8383:AA013272

R-PLACE1004868/ESTs//4.9e-70:367.94//Hs.100895:AA479308

R-PLACE1004885/Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330.78//Hs.113259:AF023456

R-PLACE1004900/EST//1.2e-46:306.86//Hs.149580:AI211881

R-PLACE1004902/Sucrose-isomaltase//0.87:254.61//Hs.2996:X63597

R-nnnnnnnnnnnn/ESTs//4.5e-75:375.96//Hs.91115:AI221563

R-PLACE1004918/ESTs//2.6e-103:519.95//Hs.143607:AI424948

R-PLACE1004930/Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532.93//Hs.17839:AF099936

R-PLACE1004934/EST//0.035:156.67//Hs.162071:AA478980

R-PLACE1004937/ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409.95//Hs.31945:AA702166

R-PLACE1004969/ESTs//9.8e-18:101.99//Hs.112837:N78013

R-PLACE1004972/ESTs//1.3e-65:337.95//Hs.75798:H29106

R-PLACE1004979/EST//1.2e-96:475.96//Hs.120158:AA208789

R-PLACE1004982/ESTs//1.0e-98:471.98//Hs.106496:AI291776

R-PLACE1004985/ESTs//2.1e-88:456.93//Hs.135050:AI420335

R-PLACE1005026

R-PLACE1005027/ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145.66//Hs.11215:N56719

R-PLACE1005046/Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297.88//Hs.153468:AB011147

R-PLACE1005052/ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543.95//Hs.18625:AI074605

R-PLACE1005066/ESTs//3.9e-92:459.96//Hs.62684:AA806103

R-PLACE1005077/Human triadin mRNA, complete cds//1.8e-05:121:89//Hs.68731:U18985

R-PLACE1005085/Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314.74//Hs.113263:AF018080

R-PLACE1005086/ESTs//1.2e-73:379.94//Hs.110128:AA584364

R-PLACE1005101/Homo sapiens (clone zap126) mRNA, 3' end of cds//8.0e-99:531.92//Hs.75437:L40401

R-PLACE1005102/ESTs//7.2e-68:493.84//Hs.10593:AI201336

R-PLACE1005108/Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232.82//Hs.155344:

U91985

R-PLACE1005111//EST//8.1e-10:189.68//Hs.136356:AA493225
 R-PLACE1005128//ESTs//1.4e-78:501.87//Hs.15093:AA203423
 R-PLACE1005146//ESTs//4.8e-93:460.97//Hs.37896:AA777349
 5 R-PLACE1005162//ESTs//7.5e-51:277.95//Hs.28838:AI089013
 R-nnnnnnnnnnn//ESTs//5.4e-75:366.97//Hs.48119:AA454227
 R-PLACE1005181//EST//0.012:172.66//Hs.147107:AI190589
 R-PLACE1005187//ESTs//5.6e-72:363.95//Hs.16577:AI022830
 R-PLACE1005206//ESTs//5.3e-48:203.88//Hs.31792:H45211
 10 R-PLACE1005232//ESTs//5.1e-41:287.84//Hs.138552:R99532
 R-PLACE1005243//ESTs//1.1e-48:348.83//Hs.113310:R16767
 R-PLACE1005261//ESTs//0.19:175.62//Hs.124337:AA829524
 R-PLACE1005266//ESTs//1.9e-22:388.66//Hs.124146:AA699633
 R-PLACE1005277//ESTs//1.5e-29:314.72//Hs.163710:AA024516
 15 R-PLACE1005287//ESTs//3.6e-95:456.98//Hs.49282:AA970322
 R-PLACE1005305//ESTs//9.9e-71:428.88//Hs.144855:AI197937
 R-PLACE1005308//ESTs//3.8e-32:173.96//Hs.58239:AA215797
 R-PLACE1005313//ESTs//5.2e-74:409.93//Hs.33368:AA206614
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537.94//Hs.136309:AB007960
 20 R-PLACE1005331//ESTs//2.1e-91:487.93//Hs.9291:AI189343
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442.97//Hs.70202:AA732975
 R-PLACE1005373//ESTs//8.0e-93:526.91//Hs.98541:N38901
 R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344.80//Hs.43681:AL022394
 R-PLACE1005409//EST//0.43:174.59//Hs.162077:AA479978
 25 R-PLACE1005453//EST//7.9e-57:330.90//Hs.162306:AA555304
 R-PLACE1005467//ESTs//2.2e-42:294.84//Hs.142257:AA188423
 R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561.86//Hs.23094:M19503
 R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549.83//Hs.78935:U29607
 R-PLACE1005480//EST//0.99:39.82//Hs.157275:AI364046
 30 R-PLACE1005481//EST//1.5e-31:281.79//Hs.132635:AI032875
 R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319.59//Hs.62705:AB000220
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277.98//Hs.28307:AF071185
 R-PLACE1005526//ESTs//2.5e-30:233.83//Hs.119304:AA443325
 35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321.69//Hs.155481:AJ006470
 R-PLACE1005530//ESTs//3.7e-81:438.92//Hs.103380:AI291325
 R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458.98//Hs.38114:N62927
 40 R-PLACE1005554//ESTs//8.8e-36:267.86//Hs.98288:AA203555
 R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345.94//Hs.7736:W81261
 R-PLACE1005574//ESTs//2.3e-27:231.83//Hs.117771:R99835
 R-PLACE1005584//ESTs//1.6e-36:188.98//Hs.152050:AY24612
 45 R-PLACE1005595//ESTs//1.6e-91:453.96//Hs.85079:AI276023
 R-PLACE1005603//ESTs//8.2e-99:533.93//Hs.96357:AI026927
 R-PLACE1005611//ESTs//5.2e-28:183.89//Hs.24941:AA261857
 R-PLACE1005623//ESTs//1.4e-102:505.96//Hs.58382:AA808964
 R-PLACE1005630
 50 R-PLACE1005639//ESTs//1.4e-51:256.98//Hs.1975:W72452
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585.93//Hs.8765:AF083255
 R-PLACE1005656//ESTs//2.7e-88:469.92//Hs.164054:AA528169
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401.66//Hs.129727:AF035587
 55 R-PLACE1005698//ESTs//0.00013:82.79//Hs.116331:AA629355
 R-PLACE1005727//EST//0.15:206.63//Hs.105002:AA448332
 R-PLACE1005730//EST//0.0014:129.70//Hs.127931:AA969259

R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]/1.3e-42:236.94//Hs.23889:AI341137

R-PLACE1005755//ESTs//2.8e-32:308.80//Hs.159821:AA524070

R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268.87//Hs.154326:D42087

R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88.98//Hs.109857:AA088385

R-PLACE1005802//ESTs//2.8e-19:208.76//Hs.9271:V30941

R-PLACE1005803//ESTs//2.6e-75:417.92//Hs.71414:AA131327

R-PLACE1005804//EST//6.5e-20:182.70//Hs.149844:AI287693

R-PLACE1005828//ESTs//3.0e-15:194.77//Hs.106236:N50058

R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435.58//Hs.75770:L41870

R-PLACE1005845//EST//5.0e-61:294.99//Hs.133202:AI050965

R-PLACE1005850//ESTs//3.4e-82:425.96//Hs.7966:AI203471

R-PLACE1005851//ESTs//2.9e-21:165.84//Hs.23607:N98305

R-PLACE1005876//ESTs//0.48:296.57//Hs.39140:AA014842

R-PLACE1005884//ESTs//0.0027:177.66//Hs.150295:AA570558

R-PLACE1005898//ESTs//1.7e-98:467.98//Hs.159475:AI339981

R-PLACE1005921//ESTs//5.8e-96:480.95//Hs.30822:AA885501

R-PLACE1005923//ESTs//1.6e-66:333.96//Hs.150890:AI341793

R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382.70//Hs.23094:M19503

R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377.93//Hs.5662:AA868361

R-PLACE1005934//ESTs//1.0e-42:251.91//Hs.25092:AA822142

R-PLACE1005936//ESTs//1.2e-88:641.94//Hs.94125:N69213

R-PLACE1005951//ESTs//1.4e-83:533.86//Hs.21148:AI183729

R-PLACE1005953

R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494.88//Hs.108117:AI097079

R-PLACE1005966//ESTs//1.1e-95:465.97//Hs.98510:AI016239

R-PLACE1005968//EST//0.26:103.66//Hs.161300:AI420897

R-PLACE1005990

R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481.74//Hs.153014:AB002353

R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593.93//Hs.111449:AI192946

R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-100:596.88//Hs.24284:AA595596

R-PLACE1006017//ESTs//1.8e-28:296.68//Hs.133350:AI056276

R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491.98//Hs.61164:AI096332

R-PLACE1006040//ESTs//1.2e-92:443.98//Hs.111680:N93765

R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213.77//Hs.139007:H74314

R-PLACE1006119//ESTs//0.14:257.61//Hs.113149:AA908904

R-PLACE1006129//ESTs//3.8e-54:285.97//Hs.18827:W68002

R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560.91//Hs.5249:U55977

R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463.59//Hs.904:U84010

R-PLACE1006157//ESTs//0.014:341.58//Hs.121773:AI357886

R-PLACE1006159//EST//0.00036:247.61//Hs.140054:AA6688925

R-PLACE1006164//ESTs//2.0e-31:362.73//Hs.141024:H07128

R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286.94//Hs.152894:AC005239

R-nnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393.96//Hs.19121:AI125280

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597.95//Hs.30464:AF091433

R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532.91//Hs.105216:AI361807

R-PLACE1006196//ESTs//3.2e-66:382.90//Hs.18665:T99507

R-PLACE1006205//EST//7.1e-79:448.96//Hs.116665:AA669114

R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77666

R-PLACE1006225//ESTs//7.2e-96:474.97//Hs.91165:AI079555
 R-PLACE1006236//ESTs//8.8e-105:535.95//Hs.7919:AI341472
 R-nnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497.95//Hs.3781:AC004142
 R-PLACE1006246//ESTs. Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532.95//Hs.41151:AI301961
 5 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499.95//Hs.31921:AB014548
 R-PLACE1006262//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321.62//Hs.53057:W67839
 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605.88//Hs.2060:L06132
 10 R-PLACE1006318//ESTs//2.4e-102:536.94//Hs.8109:AA005265
 R-PLACE1006325//ESTs//5.2e-105:518.96//Hs.102319:AI246503
 R-PLACE1006335//ESTs//5.1e-45:254.93//Hs.153585:R70900
 R-PLACE1006357//EST//6.5e-09:309.62//Hs.132493:AA923168
 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381.58//Hs.154797:D42044
 15 R-PLACE1006368//ESTs//7.9e-85:412.97//Hs.150587:AI079284
 R-PLACE1006371//ESTs//7.7e-74:442.88//Hs.143671:W61053
 R-PLACE1006382
 R-PLACE1006385//ESTs//5.3e-06:346.61//Hs.163706:AA515748
 R-PLACE1006412//EST//7.7e-46:306.96//Hs.149580:AI281881
 20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551.69//Hs.154103:AF061258
 R-PLACE1006438//ESTs//1.1e-77:284.86//Hs.24545:AI278629
 R-PLACE1006445//ESTs//4.4e-53:259.99//Hs.24481:AA573139
 R-PLACE1006469//ESTs//9.4e-102:482.98//Hs.7218:AA936961
 R-PLACE1006470//ESTs//1.0:271.57//Hs.144517:AA938297
 25 R-PLACE1006482//ESTs//4.0e-61:354.92//Hs.51305:T47418
 R-PLACE1006492//EST//1.8e-09:48.91//Hs.144451:AA827722
 R-PLACE1006506//ESTs//0.012:161.61//Hs.145333:AI251374
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415.63//Hs.48824:D87717
 R-PLACE1006531//ESTs//5.6e-31:213.87//Hs.125153:AA453723
 30 R-PLACE1006534//ESTs//6.5e-101:512.95//Hs.27763:W46368
 R-PLACE1006540//ESTs//7.3e-40:320.79//Hs.121659:H02532
 R-PLACE1006552//EST//0.38:418.56//Hs.140470:AA765214
 R-PLACE1006598//ESTs//4.0e-80:409.95//Hs.142868:AI128443
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//9.3e-118:590.95//Hs.155377:U97670
 35 R-PLACE1006617//ESTs//8.1e-31:246.83//Hs.139128:AA205322
 R-PLACE1006626//ESTs//0.90:98.68//Hs.96322:AA541615
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315.78//Hs.101359:AB002384
 R-PLACE1006640//ESTs//3.7e-26:137.100//Hs.32672:W16522
 40 R-PLACE1006673//Interleukin 10//8.4e-47:330.83//Hs.2180:M57627
 R-PLACE1006678//ESTs//1.1e-13:87.98//Hs.34035:D87736
 R-PLACE1006704//ESTs//2.6e-65:394.89//Hs.30582:D12214
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486.98//Hs.12472:AF038172
 R-PLACE1006754//EST//1.0e-61:381.89//Hs.14727:T83861
 45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394.93//Hs.7252:AF070622
 R-PLACE1006779//ESTs//1.4e-69:405.90//Hs.136235:AA262658
 R-PLACE1006782//EST//1.8e-25:197.86//Hs.137257:N33234
 R-PLACE1006792//ESTs//1.8e-43:317.84//Hs.139190:N55515
 R-PLACE1006795//ESTs//6.4e-68:350.95//Hs.11092:AA916335
 50 R-PLACE1006800//ESTs//1.9e-55:268.100//Hs.126695:AA917989
 R-PLACE1006805//ESTs//6.6e-91:484.93//Hs.94262:AA768847
 R-PLACE1006815//ESTs//2.1e-49:364.83//Hs.142031:AA809159
 R-PLACE1006819//ESTs. Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-87:481.92//Hs.141263:H64113
 55 R-PLACE1006829//ESTs//5.7e-43:332.83//Hs.19906:AA456933
 R-PLACE1006860//ESTs//0.96:138.63//Hs.136649:AA-828359
 R-PLACE1006867//ESTs//1.4e-98:478.97//Hs.10299:N35008
 R-PLACE1006878//EST//8.4e-48:243.97//Hs.54970:N93536

R-PLACE1006883/ESTS//3.1e-46:300.88/Hs.162404.AA573131
R-nnnnnnnnnnnn/ESTS//3.0e-95:496.94/Hs.47546.AA181348
R-PLACE1006904/ESTS//5.8e-18:304.68/Hs.125816.AA806089
R-PLACE1006917/Endothelin receptor type B//0.00012:451.60/Hs.82002.D13168
5 R-PLACE1006932/ESTS//4.6e-56:285.96/Hs.114727.AI975194
R-PLACE1006935/ESTS//3.6e-12:157.73/Hs.161714.AA229078
R-nnnnnnnnnnnn/Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494.63/Hs.36927.D86956
R-PLACE1006961/Tyrosine aminotransferase/plak2.5e-46:471.74/Hs.2999.X52520
R-PLACE1006962/ESTS, Moderately similar to plakophilin 2b [H.sapiens]/9.0e-29:324.68/Hs.154257.AI275982
10 R-PLACE1006966/ESTS//4.5e-99:470.99/Hs.46913.AI017636
R-PLACE1006989/ESTS//2.2e-68:353.97/Hs.14394.R61257
R-PLACE1007014/ESTS//3.4e-86:457.94/Hs.129819.AA938366
R-PLACE1007021/ESTS//1.6e-93:539.90/Hs.7111.U55971
R-PLACE1007045/Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584.82/Hs.23094.M19503
15 R-PLACE1007053/ESTS//4.2e-85:550.88/Hs.7984.AI202575
R-PLACE1007097/ESTS//6.4e-78:493.86/Hs.56406.N91027
R-PLACE1007105/ESTS//5.3e-70:381.91/Hs.22605.N74202
R-PLACE1007111/ESTS//8.6e-75:358.99/Hs.145629.AA398646
R-PLACE1007112/ESTS//6.9e-69:371.94/Hs.71922.AA148417
20 R-PLACE1007132/ESTS//1.2e-36:373.69/Hs.10762.W28948
R-PLACE1007140/ESTS//1.7e-70:360.96/Hs.56179.W56794
R-PLACE1007178/EST//0.68:85.65/Hs.14701O.IA184765
R-PLACE1007226/ESTS//3.1e-78:452.90/Hs.8033.N49498
R-PLACE1007238/ESTS//5.2e-70:362.95/Hs.85636.AA740619
25 R-PLACE1007239/Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:
89/Hs.80598.D50495
R-PLACE1007242/ESTS//1.2e-80:390.98/Hs.117325.AA699450
R-PLACE1007243/ESTS, Weakly similar to transporter protein [H. sapiens]/3.7e-73:357.98/Hs.18272.N78499
R-PLACE1007257/Homo sapiens mRNA for dia-156 protein//4.3e-85:487.91/Hs.121556.Y15909
30 R-PLACE1007274/ESTS//4.3e-79:430.93/Hs.146023.AI275071
R-PLACE1007276/ESTS//1.5e-33:338.74/Hs.142850.R38419
R-PLACE1007282/ESTS//4.8e-98:532.93/Hs.10071.AA100812
R-PLACE1007286/Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518.74/Hs.154326.D42087
35 R-PLACE1007301
R-PLACE1007317
R-PLACE1007342
R-PLACE1007346/Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:
91/Hs.76596.AF096870
R-PLACE1007367/ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/2.2e-98:
488:96/Hs.24359.AA699594
40 R-PLACE1007375/ESTS//2.3e-67:375.92/Hs.33368.AA206614
R-PLACE1007386/ESTS//0.020:242:62/Hs.42768.AI129945
R-PLACE1007402/ESTS//1.6e-91:441.97/Hs.26243.AA455877
R-PLACE1007409/Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590.94/
45 Hs.14387.AF093771
R-PLACE1007416/ESTS, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]/3.8e-115:579.95/Hs.
72165.AI243857
R-PLACE1007450/Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:
80/Hs.97203.U83171
50 R-PLACE1007452/EST//2.5e-42:386.77/Hs.140562.AA826514
R-PLACE1007460/ESTS//4.9e-87:434.95/Hs.28472.AI028230
R-PLACE1007478
R-PLACE1007484/ESTS//6.8e-08:64.92/Hs.100251.AA535975
R-PLACE1007488/Dysmorphin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,
55 DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS270//0.26:411:60/Hs.79012.M18533
R-PLACE1007507/ESTS//2.2e-111:136.76/Hs.128815.AA687272
R-PLACE1007511/ESTS, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]/1.5e-41:261:
89/Hs.9029.W57657

- R-PLACE1007524//ESTs//5.8e-45:297.87//Hs.154923:AA491377
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422.75//Hs.154326:D42087
 R-PLACE1007544//ESTs//8.4e-59:327.93//Hs.27410:N25612
 R-PLACE1007547//EST//0.00010:107.71//Hs.146867:AI161404
 5 R-PLACE1007557//ESTs//1.6e-43:356.79//Hs.44702:AI148840
 R-PLACE1007583//ESTs//1.7e-41:214.97//Hs.155071:AA584257
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554.93//Hs.21838:AF038179
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)/0.54:161.65//Hs.76506:J02923
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537.94//Hs.151046:AF038176
 10 R-PLACE1007632
 R-PLACE1007645//ESTs//0.99:187.62//Hs.163453:AI344106
 R-PLACE1007649//ESTs//2.2e-108:561.94//Hs.24398:AI262946
 R-PLACE1007677//ESTs. Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//
 9.0e-37:190.97//Hs.23437:AA707331
 15 R-PLACE1007688//ESTs//7.5e-79:409.95//Hs.6166:AI376944
 R-PLACE1007690//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]
 //3.4e-61:384.89//Hs.92918:AA133274
 R-PLACE1007697//ESTs. Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501.88//Hs.
 91251:U66685
 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307.59//Hs.54481:D86407
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374.96//Hs.4812:
 AF061243
 R-PLACE1007725//ESTs. Weakly similar to No definition line found [C.elegans]//3.1e-39:253.88//Hs.108797:
 AA476815
 25 R-PLACE1007729//ESTs//2.7e-44:392.79//Hs.142375:AA398619
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556.89//Hs.153121:
 AB014585
 R-PLACE1007737//ESTs//1.1e-41:345.80//Hs.114671:N39322
 R-PLACE1007743//ESTs//2.8e-17:98.100//Hs.124258:AA976778
 30 R-PLACE1007746//ESTs//5.3e-69:413.90//Hs.5297:AA156903
 R-PLACE1007791//ESTs. Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//
 8.6e-27:143.98//Hs.144194:AA706337
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428.76//Hs.23094:M 9503
 R-PLACE1007810//ESTs//5.9e-15:143.82//Hs.126257:AI279044
 35 R-PLACE1007829//ESTs//2.2e-22:190.84//Hs.142707:W24050
 R-PLACE1007843//ESTs//5.3e-110:556.95//Hs.107287:AI308839
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525.91//Hs.23094:M19503
 R-PLACE1007852//ESTs//4.5e-14:174.75//Hs.153419:N52017
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574.94//Hs.28020:
 40 AB018309
 R-PLACE1007866//EST//1.8e-48:262.96//Hs.141009:H01178
 R-PLACE1007877//ESTs//1.2e-94:478.96//Hs.5999:AI207832
 R-PLACE1007897//ESTs//2.3e-92:437.99//Hs.122843:AI189060
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460.95//Hs.
 45 92381:AB007956
 R-PLACE1007946//ESTs//2.8e-28:172.78//Hs.126784:AA521510
 R-PLACE1007954//ESTs//6.1e-72:366.95//Hs.27842:AI217966
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509.96//Hs.
 5671:AF084530
 50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:
 465.93//Hs.78106:AF079529
 R-PLACE1007969//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534.99//Hs.44268:AA45900
 R-PLACE1007990//ESTs. Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
 //3.8e-97:493.95//Hs.6141:U69564
 55 R-PLACE1008000//ESTs//0.00013:241.65//Hs.44369:AI206835
 R-PLACE1008002//ESTs//2.2e-83:397.98//Hs.28780:AI263612
 R-PLACE1008044//ESTs. Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]
 //2.0e-115:575.95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:A1054269
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
 R-nnnnnnnnnnnn
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//
 Hs.146477:AI128445
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-
 41:448:72//Hs.139007:H74314
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:
 30 536:87//Hs.7570:W31010
 R-nnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
 R-PLACE1008532
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
 R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:
 AA778649
 R-nnnnnnnnnnnn
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
 55 R-PLACE10086507//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.
 147967:AF044333
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

- 76//Hs.1361:M55053
 R-PLACE1008715//EST//0.63:114.64//Hs.121353:AA758600
 R-PLACE1008748//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303
- 5 R-PLACE1008757//ESTs//1.4e-45:226.99//Hs.22822:H06408
 R-PLACE1008790//ESTs//0.035:67.76//Hs.153554:AI286313
 R-PLACE1008798//ESTs//4.9e-59:285.99//Hs.49018:N79930
 R-PLACE1008807//ESTs//1.7e-82:413.96//Hs.130745:AA573217
 R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905
- 10 R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490.93//Hs.110454:H11810
 R-PLACE1008851//ESTs//2.4e-84:421.95//Hs.158893:AI374828
 R-nnnnnnnnnnnnn
- 15 R-PLACE1008867//ESTs//1.1e-77:400.95//Hs.44198:AI093502
 R-PLACE1008887//Oxytocin receptor//1.1e-43:601.67//Hs.2820:X64878
 R-PLACE1008902//ESTs//0.023:208.61//Hs.154164:AI246893
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344.89//Hs.62318:AB018308
 R-PLACE1008925//ESTs//0.17:294.57//Hs.105113:AA457018
- 20 R-PLACE1008934//ESTs//2.0e-61:339.92//Hs.100448:AA622653
 R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488.63//Hs.15780:U66680
 R-PLACE1008947//ESTs//1.3e-81:385.99//Hs.71574:AI376573
 R-PLACE1009020//ESTs//2.9e-79:419.94//Hs.121816:AA775419
- 25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434.94//Hs.34780:AJ003112
 R-PLACE1009039//ESTs//2.8e-83:448.92//Hs.129179:AA988520
 R-PLACE1009045//ESTs//1.6e-64:318.97//Hs.103423:AA814195
 R-PLACE1009048//ESTs//2.7e-17:403.63//Hs.149343:AI249139
 R-PLACE1009050//ESTs//2.0e-88:475.92//Hs.122925:AA909008
- 30 R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555.96//Hs.9663:AA527142
 R-PLACE1009090//ESTs//5.0e-13:175.75//Hs.140608:N53448
 R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161.63//Hs.77608:AL021546
 R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63.84//Hs.39943:AA203136
- 35 R-PLACE1009110//EST//5.8e-17:307.65//Hs.117264:AA682549
 R-PLACE1009111//ESTs//1.9e-57:349.90//Hs.11260:N98983
 R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501.94//Hs.11123:AA703945
 R-PLACE1009150//LAMIN B1//0.064:393.60//Hs.89497:L37747
- 40 R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163.82//Hs.93332:AA811920
 R-PLACE1009158//ESTs//0.30:149.65//Hs.155796:R80005
 R-PLACE1009166//ESTs//3.3e-34:292.77//Hs.140255:AA708322
 R-PLACE1009172//EST//8.9e-21:364.67//Hs.142557:AA64948
- 45 R-PLACE1009174//ESTs//2.9e-18:274.70//Hs.139241:AA283707
 R-PLACE1009183//ESTs//2.3e-44:297.87//Hs.136839:H93717
 R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572.94//Hs.54943:Z78396
 R-PLACE1009190//ESTs//2.6e-53:318.90//Hs.25245:AA176701
- 50 R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195.92//Hs.104247:X98248
 R-PLACE1009230//ESTs//3.0e-31:153.92//Hs.124116:AA772680
 R-PLACE1009246//ESTs//2.7e-90:488.92//Hs.10706:AA909018
 R-PLACE1009308//ESTs//0.022:46.97//Hs.36545:AA075423
 R-PLACE1009319//ESTs//7.7e-99:533.92//Hs.109654:N91279
- 55 R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578.82//Hs.23094:M19503
 R-PLACE1009335//EST//1.3e-64:311.99//Hs.130558:AI004397
 R-PLACE1009338//ESTs//6.0e-70:386.93//Hs.3542:AI015782
 R-PLACE1009368//ESTs//1.4e-18:107.98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.e-36:31376/Hs.24608:AA161260
R-PLACE1009388//EST/I/4.e-11:101:83//Hs.147074:AI188883
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186
R-nnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:P72798
5 R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255
R-PLACE1009434//EST/I/3.e-15:109:74//Hs.103742:U48632
R-PLACE1009443//EST/I/7.5e-61:302:98//Hs.157787:AI361269
R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427
10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:AC004531
R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
R-PLACE1009493//ESTs//4.5e-14:150:73//Hs.143918:AA699596
R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698
15 R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131
R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263
R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.sapiens]/0.002:56:91//Hs.12151:AA001818
20 R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:AB014535
R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735
R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482
25 R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
R-PLACE1009621//EST/I/0.99:26:60//Hs.149300:AI243338
R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858
R-PLACE1009637//EST/R/8.7e-90:442:97//Hs.121372:AA758701
R-PLACE1009639//EST/R/8.5e-49:279:93//Hs.117447:R27213
30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:AB011159
R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]/9.9e-62:483:79//Hs.140416:AA778649
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534
35 R-PLACE1009708//ESTs//3.Oe-94:471:96//Hs.40091:N48582
R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]/4.2e-98:529:92//Hs.3945:AA004210
R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]/6.8e-85:489:89//Hs.26194:AA033889
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024
40 R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989
R-nnnnnnnnnnnn/Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Ci-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996
45 R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868
R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748
R-PLACE1009886//EST/I/0.54:153:64//Hs.144281:AA081328
R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031
50 R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]/1.6e-114:594:94//Hs.67466:AI219740
R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563
R-PLACE1009924//EST/I/2.e-42:216:98//Hs.31742:H20276
R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317
55 R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543
R-PLACE1009947//Keratin 9//I.0.273:61//Hs.2783:Z29074
R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540
R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs/I/3.e-103.575.91/Hs.71218:C75347
R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286.86/Hs.155646:AF088219
R-PLACE1010023//ESTs, Weakly similar to C2F2.7 gene product [C.elegans]/1.7e-17:137.86/Hs.7049:
A1141736
R-PLACE1010031//ESTs/I/0.22:191.62/Hs.127787:AA832204
R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]/
7.6e-104:546.94/Hs.8215:AA521150
R-PLACE1010069//ESTs/I/0.99:173.59/Hs.21415:A1150905
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds/I/1.5e-88:543.88/Hs.
11183AF065482
R-PLACE1010076//ESTs/I/3.4e-106:530.95/Hs.28005:AA604375
R-PLACE1010083//ESTs/I/4.1e-65:395.88/Hs.6103:AA496424
R-PLACE1010089//ESTs/I/1.6e-70:348.97/Hs.9011:AA418615
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]/I/2.8e-104:565.92/Hs.11469:
U69567
R-PLACE1010102//ESTs/I/7.7e-50:311.89/Hs.5518:A1052015
R-PLACE1010105//ESTs/I/6.0e-94:483.94/Hs.62684:AA806103
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]/I/1.6e-107:575.93/Hs.48301:AA122270
R-PLACE1010134//EST/I/8.5e-59:314.94/Hs.135005:AI095130
R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79/I/0.52:351.56/Hs.48714:M90359
R-PLACE1010152//ESTs/I/1.9e-40:240.90/Hs.17054:A1139897
R-PLACE1010181//ESTs/I/3.6e-64:307.99/Hs.154163:AJ003313
R-PLACE1010194//ESTs/I/2.7e-70:366.96/Hs.5301:T58466
R-PLACE1010202//ESTs/I/0.57:120.67/Hs.58873:W95037
R-PLACE1010231
R-PLACE1010261//EST/I/6.9e-50:251.98/Hs.148208:AA897478
R-PLACE1010270//ESTs/I/1.9e-87:430.96/Hs.25252:AI079545
R-PLACE1010274//ESTs/I/1.9e-57:439.81/Hs.30078:H04535
R-PLACE1010293//ESTs/I/8.1e-41:310.81/Hs.146811:AA410788
R-PLACE1010321//ESTs/I/5.7e-50:246.99/Hs.151445:AA351081
R-PLACE1010324//ESTs/I/0.00025:377.60/Hs.97430:AA398568
R-PLACE1010329//Small inducible cytokine A5 (RANTES)/I/2.4e-40:300.82/Hs.155646:AF088219
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]/I/9.9e-
32:190.77/Hs.152369:AA504818
R-PLACE1010362//ESTs/I/8.2e-86:404.99/Hs.25625:AA669327
R-PLACE1010364//ESTs/I/1.5e-105:556.93/Hs.12229:AA149594
R-PLACE1010383//Homo sapiens mRNA for putative lipoid acid synthetase, partial/I/4.9e-35:166.86/Hs.53531:
AJ224162
R-PLACE1010401//ESTs/I/2.3e-85:450.93/Hs.23193:AA418152
R-PLACE1010481//EST/I/0.012:280.59/Hs.5579:AI392816
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds/I/2.4e-89:438.96/Hs.13313:
AF039081
R-PLACE1010492
R-PLACE1010522//EST/I/0.43:82.68/Hs.89303:AA284031
R-nnnnnnnnnnnn/ESTs/I/3.4e-36:228.89/Hs.128724:AA215455
R-PLACE1010562//ESTs/I/4.8e-68:408.90/Hs.17244:W86306
R-PLACE1010579//EST/I/0.015:193.63/Hs.67093:C14033
R-PLACE1010580//ESTs/I/2.4e-93:445.98/Hs.127325:AA234116
R-PLACE1010599
R-PLACE1010616//ESTs/I/2.9e-101:497.97/Hs.142197:AA573418
R-PLACE1010622//ESTs/I/7.1e-23:157.91/Hs.159877:W57895
R-PLACE1010624//ESTs/I/1.4e-89:428.98/Hs.116561:AA658475
R-PLACE1010628//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/I/6.4e-74:
391.95/Hs.163495:W57637
R-PLACE1010629//ESTs/I/5.8e-75:359.99/Hs.123630:AI250805
R-PLACE1010630//ESTs/I/9.5e-101:519.94/Hs.77873:AA371719
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds/I/8.3e-94:497.93/Hs.10801:AB011102
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBST13 [Mus musculus]/I/4.8e-83:467:

- 91//Hs.22383:R51067
 R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
 PRECURSOR [D.melanogaster]/8.3e-103:538:94//Hs.105794:AA701659
 R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152/4.8e-46:531:71//Hs.55452:AC003973
 5 R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//
 Hs.46440:U21943
 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:
 95//Hs.50758:AF092564
 10 R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189
 R-PLACE1010743
 R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-
 94:442:96//Hs.3688:AF069250
 R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024
 15 R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]/7.6e-111:575:
 94//Hs.10260:AI126627
 R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558
 R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203
 R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896
 R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472
 20 R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048
 R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]/1.4e-71:326:92//Hs.3385:N25917
 R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090
 R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:
 AB011182
 25 R-PLACE1010891
 R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983
 R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023
 R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)/0.25:190:61//Hs.75716:Y00630
 R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093
 30 R-PLACE1010925//ESTs//1.1e-82:471:95//Hs.17448:AI125479
 R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126
 R-nnnnnnnnnnnnn/Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:
 AF064244
 R-PLACE1010944
 35 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
 R-PLACE1010954//Small inducible cytokine A5 (RANTES)/8.8e-51:278:93//Hs.155464:AF088219
 R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]/1.0e-103:565:
 92//Hs.23259:AA532437
 R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
 40 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
 R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
 R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
 45 R-PLACE1011056//Small inducible cytokine A5 (RANTES)/3.5e-38:285:82//Hs.155464:AF088219
 R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
 R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.6e-54:
 398:84//Hs.108740:W20094
 R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478
 50 R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587
 R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]/3.0e-105:552:93//Hs.31257:
 AA875998
 R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
 R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
 55 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
 R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/3.4e-85:442:
 95//Hs.136910:AA810782
 R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

R-PLACE1011219//ESTs//7.6e-96:504.93//Hs.124834:AI138671
R-PLACE1011221//ESTs//5.2e-23:241.78//Hs.28761:AA203299
R-PLACE1011229//ESTs//1.9e-90:461.95//Hs.132288:AI027693
R-PLACE1011263//ESTs//6.6e-56:321.93//Hs.158787:V79602
5 R-PLACE1011273//ESTs//0.016:131.65//Hs.140466:AA766772
R-PLACE1011291//EST//8.7e-47:267.91//Hs.158806:AI376913
R-PLACE1011296//EST//2.7e-38:225.92//Hs.160934:AI376849
R-PLACE1011310//ESTs//9.1e-37:196.96//Hs.39328:H71807
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486.58//Hs.83572:U79291
10 R-PLACE1011332//ESTs//8.4e-44:217.99//Hs.101365:R60578
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452.97//Hs.144194:AA706337
R-PLACE1011375//ESTs//2.2e-35:195.96//Hs.106486:H11376
R-PLACE1011399//ESTs//0.00096:224.67//Hs.151643:AA0001194
15 R-PLACE1011419//ESTs//4.9e-50:267.95//Hs.7045:AA167337
R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600.94//Hs.10801:AB011102
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310.76//Hs.138488:AB014607
20 R-PLACE1011465//ESTs//4.5e-86:471.93//Hs.144519:R70887
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515.96//Hs.111138:AB018255
R-PLACE1011492//ESTs//1.7e-96:488.95//Hs.116555:AA639278
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0.193:60//Hs.28197:AF035294
25 R-PLACE1011520//ESTs//6.8e-99:477.97//Hs.85077:AA968576
R-PLACE1011563//ESTs//1.4e-94:514.92//Hs.16471:AA206421
R-PLACE1011567//EST//2.8e-89:417.100//Hs.149770:AI285985
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)/4.7e-55:267.81//Hs.8597:L11672
R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168.61//Hs.78344:AF001548
30 R-PLACE1011635//ESTs//2.5e-67:332.98//Hs.108194:AA780067
R-PLACE1011641//ESTs//2.5e-71:138.100//Hs.153085:AA993965
R-PLACE1011643//EST//1.9e-18:181.78//Hs.160879:AI361900
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414.91//Hs.78019:AF070535
R-PLACE1011650//EST//5.8e-18:118.92//Hs.124486:AA846036
35 R-PLACE1011664//Retin (Reed-Steinberg cell-expressed intermediate filament-associated protein)/0.50:178:62//Hs.31638:X64838
R-PLACE1011675
R-PLACE1011682//ESTs//2.4e-90:465.94//Hs.57830:AI312025
R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410.83//Hs.23094:M19503
40 R-PLACE1011725//ESTs//2.0e-70:340.98//Hs.161725:AA251392
R-PLACE1011729//ESTs//7.5e-19:180.79//Hs.119516:AA443426
R-PLACE1011749//Myelin oligodendrocyte glycoprotein [alternative products]//7.3e-40:361.77//Hs.53217:Z48051
R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319.76//Hs.103948:K00627
45 R-PLACE1011778//ESTs//8.0e-70:372.94//Hs.46765:AA521080
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279.85//Hs.13572:AF068179
R-PLACE1011858//ESTs//2.6e-69:396.91//Hs.55220:U11563
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439.80//Hs.22271:D26067
R-PLACE1011875//ESTs//9.0e-88:420.98//Hs.70897:AA987648
50 R-PLACE1011891//ESTs//3.9e-17:97.100//Hs.84698:AA725913
R-PLACE1011896//ESTs//2.8e-23:176.84//Hs.121540:AI275497
R-PLACE1011922//ESTs//6.6e-35:415.73//Hs.10972:AA164268
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546.92//Hs.3838:AF059617
55 R-PLACE1011962//ESTs//3.3e-49:294.90//Hs.106800:AI031969
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284.63//Hs.124102:AA701285
R-PLACE1011982//ESTs//2.9e-51:291.93//Hs.20792:R14890

- R-PLACE1011995//ESTs//4.5e-39:304.81//Hs.138852:AA284247
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540.95//Hs.88756:AB018256
- 5 R-PLACE2000003//ESTs//2.0e-103:488.98//Hs.8341:AA490069
 R-PLACE2000007//ESTs//2.4e-110:564.95//Hs.65135:W89120
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524.95//Hs.21811:AF091080
- 10 R-PLACE2000015//ESTs//7.1e-111:543.96//Hs.32178:AA083211
 R-PLACE2000017//EST//8.2e-46:404.79//Hs.133006:AI049504
 R-PLACE2000021//EST//4.5e-19:221.71//Hs.150830:AI302868
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355.79//Hs.154069:U06452
- 15 R-PLACE2000034//ESTs//2.2e-21:314.70//Hs.107697:W29013
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514.72//Hs.96247:X95073
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358.81//Hs.159523:AF001622
- 20 R-PLACE2000050//ESTs//4.5e-65:322.98//Hs.155820:N67652
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429.72//Hs.153468:AB011147
 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296.86//Hs.40100:AB002390
- 25 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550.95//Hs.9443:AF027219
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372.80//Hs.13572:AF068179
 R-PLACE2000100//ESTs//8.8e-42:281.86//Hs.150727:AI292236
- 30 R-PLACE2000103//ESTs//4.7e-97:518.93//Hs.118727:W26941
 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127.71//Hs.42400:AF022789
 R-PLACE2000115//ESTs//7.8e-93:458.96//Hs.104520:AA481662
- 35 R-PLACE2000132//ESTs//3.8e-69:409.91//Hs.98502:AA433988
 R-PLACE2000136//ESTs//6.2e-05:274.61//Hs.114067:AA701558
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302.85//Hs.118401:AB011134
- 40 R-PLACE2000164//ESTs//6.3e-106:506.98//Hs.16390:AI052357
 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326.79//Hs.155464:AF088219
 R-PLACE2000172//ESTs//9.6e-43:232.94//Hs.6709:AI379778
- 45 R-PLACE2000176//EST//1.6e-24:154.91//Hs.157734:AI360292
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292.90//Hs.22271:D26067
 R-PLACE2000216//ESTs//0.0041:166.64//Hs.159476:AI382378
- 50 R-PLACE2000223//ESTs//0.49:171.60//Hs.86154:AA207191
 R-PLACE2000235//ESTs//2.9e-39:264.85//Hs.136839:H93717
 R-PLACE2000246//NAD(P)H:menadiol oxidoreductase//4.0e-44:331.82//Hs.80706:M81600
- 55 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311.81//Hs.84123:AB002363
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422.98//Hs.9740:AI004779
- 60 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380.92//Hs.107365:AA720664
 R-PLACE2000305//ESTs//2.6e-43:413.75//Hs.118732:AI344055
 R-PLACE2000317//ESTs//2.8e-92:501.92//Hs.28432:R83380
- 65 R-PLACE2000335//ESTs//4.3e-32:300.77//Hs.163035:AA748058
 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117.73//Hs.42400:AF022789
- 70 R-PLACE2000347//ESTs//1.6e-30:214.86//Hs.135272:AI347618
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288.86//Hs.140090:U09848
 R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392.82//Hs.89887:D38081
- 75 R-PLACE2000371//ESTs//3.6e-81:409.97//Hs.155138:AA158731
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186.62//Hs.101516:AB018277
 R-PLACE2000379//ESTs//3.4e-10:228.64//Hs.57842:W63781
 R-PLACE2000394//ESTs//6.7e-41:462.74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373.74//Hs.155184:AA573189
R-PLACE2000399
R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424
5 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941
R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739
R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287.88//Hs.153563:AF011333
R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002
10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986
R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887
R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
15 R-PLACE2000458//ESTs//6.8e-82:473:96//Hs.115897:AA156638
R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228
R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838
R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:
20 AB011147
R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763
R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727
25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739
R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369
R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142
R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815
30 R-PLACE3000158//ESTs//1.2e-19:192:79//Hs.131350:AA805223
R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//
Hs.31532:H18272
R-PLACE3000157
R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
35 R-PLACE3000160
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
R-PLACE3000194
R-PLACE3000197//ESTs//1.4e-38:197:98//Hs.146341:AI269930
R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.
40 131370:AA927516
R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476
R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717
45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878
R-PLACE3000242//Human thornin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-
110:549:95//Hs.13692:AA632002
50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:
82//Hs.97203:U83171
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-
55 plete cds//4.0e-59:456:80//Hs.108966:U48696
R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

- 114531:N74103
R-PLACE3000331/Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315
- 5 R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837
R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688
R-PLACE3000350/Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888
- 10 R-PLACE3000363
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534
- 15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570
R-PLACE3000400//ESTs//8.3e-05:130:63//Hs.17697:AA287528
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160
R-PLACE3000405/Human hSLIM15 mRNA for hSLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108
- 20 R-PLACE3000406/Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519
- 25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA84461
R-PLACE3000475/Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227
- 30 R-PLACE4000014/Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292
- 35 R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739
R-PLACE4000100
R-PLACE4000106/Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931
- 40 R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985
R-PLACE4000129/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969
- 45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582
R-PLACE4000156/Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186
- 50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216
- 55 R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586
R-PLACE4000270/Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103.68//Hs.144438:AA780782
 R-PLACE4000320//EST//2.7e-44:298.85//Hs.162404:AA573131
 R-PLACE4000323//ESTs//8.8e-38:178.79//Hs.155475:AA761454
 R-PLACE4000326//ESTs//7.4e-103:516.96//Hs.55042:AA150460
 5 R-PLACE4000344//ESTs//9.9e-94:463.96//Hs.100057:AA001414
 R-PLACE4000367//ESTs//0.81:102.73//Hs.107692:H38478
 R-PLACE4000369//ESTs//1.5e-69:390.92//Hs.13733:AA418856
 R-PLACE4000379//ESTs//1.3e-67:373.91//Hs.48569:AA905425
 10 R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379.78//Hs.152369:AA504818
 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482.83//Hs.140416:AA778649
 R-PLACE4000401//ESTs//1.3e-18:151.84//Hs.150355:AI273502
 R-PLACE4000411//ESTs//1.1e-108:543.96//Hs.23901:AA169780
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530.98//Hs.12003:AA643063
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409.72//Hs.1361:M55053
 R-PLACE4000489//ESTs//5.0e-70:342.98//Hs.72865:AI380932
 20 R-PLACE4000494//EST&I//1.4e-109:525.98//Hs.22539:AI334210
 R-PLACE4000522//ESTs//6.3e-88:471.93//Hs.8121:AA521290
 R-PLACE4000548//ESTs//3.3e-86:441.96//Hs.5070:AA149527
 R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425.76//Hs.23590:U59185
 25 R-THYRO1000026//ESTs//2.6e-42:331.82//Hs.137875:AA993532
 R-THYRO1000034//ESTs//2.1e-43:214.100//Hs.153018:AI243524
 R-THYRO1000035//ESTs//7.6e-52:325.90//Hs.49817:AA001249
 R-THYRO1000040//ESTs//1.7e-94:459.98//Hs.48712:AI027889
 R-THYRO1000070//ESTs//6.7e-43:283.86//Hs.37573:H59651
 30 R-THYRO1000072//ESTs//1.3e-57:313.96//Hs.127827:H13438
 R-THYRO1000085//ESTs//1.1e-90:439.98//Hs.150539:AA908435
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344.79//Hs.153014:AB002353
 R-THYRO1000107//Interleukin 10//2.8e-43:292.84//Hs.2180:M57627
 35 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413.80//Hs.140385:AA773359
 R-THYRO1000121//EST//0.24:78.74//Hs.156632:AI345108
 R-THYRO1000124//ESTs//2.8e-86:428.96//Hs.141634:AI122764
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449.96//Hs.87619:AF087142
 40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486.77//Hs.24164:N95217
 R-THYRO1000156//ESTs//6.1e-36:344.75//Hs.70279:AA757426
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278.84//Hs.154103:AF061258
 45 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554.96//Hs.18894:AA910946
 R-THYRO1000186//ESTs//1.0e-44:339.83//Hs.155184:AA573189
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305.81//Hs.155464:AF088219
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301.85//Hs.155464:AF088219
 50 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535.97//Hs.43445:AJ005698
 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559.97//Hs.79672:AB014552
 R-THYRO1000206//ESTs//3.1e-90:507.90//Hs.32456:W29063
 R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-72:357.98//Hs.140002:AA635349
 55 R-THYRO1000241//Homo sapiens mRNA for KIAA0888 protein, complete cds//7.8e-69:524.82//Hs.141874:AB014588
 R-THYRO1000242//ESTs//4.2e-27:222.85//Hs.77554:W87927

R-THYRO1000253/Sialophorin (gpl.115, leukosialin, CD43)/7.3e-40:318.80/Hs. 80738.X52075
R-THYRO1000270/ESTs/1.9e-99:531.94/Hs.17767.N62925
R-THYRO1000279/EST/1.2.7e-54:266.99/Hs.149527.AI280674
R-THYRO1000288/Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566.91/Hs.25846.AB016068
R-THYRO1000320/POLYSPINS LOCUS PROTEIN 1//1.0:321.58/Hs.74648.M73547
R-THYRO1000327/Autocrine motility factor receptor/9.2e-54:289.93/Hs.80731.M63175
R-THYRO1000343/Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559.96/Hs.12002:AB018333
R-THYRO1000358/Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317.87/Hs.7833.U29091
R-THYRO1000368/ESTs/4.7e-88:430.98/Hs.146085.AA021064
R-nnnnnnnnnnnn/ESTs/1.0:253.57/Hs.128783.AA436250
R-THYRO1000387/Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds/4.6e-69:294.84/Hs.151614.AF032456
R-THYRO1000394/Thromboxane A2 receptor/4.1e-40:232.87/Hs.89887.D38081
R-THYRO1000395/ESTs/3.3e-20:160.83/Hs.101570:AA050429
R-THYRO1000401/ESTs/1.3e-109:516.99/Hs.78524.AI140601
R-THYRO1000438/ESTs/2.1e-48:360.83/Hs.141203:W52638
R-THYRO1000452/ESTs, Weakly similar to No definition line found [C.elegans]/(8.5e-40:239.90/Hs.84009:AI309761
R-THYRO1000471/ESTs/3.3e-36:302.80/Hs.70279:AA757426
R-THYRO1000484/Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479.75/Hs.17630:AB018280
R-THYRO1000488/Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471.94/Hs.28719:AB015333
R-THYRO1000501/ESTs/L5e-46:287.89/Hs.125300.R62360
R-THYRO1000502/ESTs/1.7e-08:63.96/Hs.116319:AI208005
R-THYRO1000505/ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286.96/Hs.105861.AI206965
R-THYRO1000558/ESTs/1.7e-95:454.99/Hs.125063:AA648511
R-THYRO1000569/ESTs/3.2e-89:463.94/Hs.20555:W22193
R-THYRO1000570/ESTs/2.8e-97:471.97/Hs.8245:AA115485
R-nnnnnnnnnnnn/Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533.97/Hs.151411:AF075587
R-THYRO1000596/ESTs/3.1e-99:527.94/Hs.6084:AA045247
R-THYRO1000602/EST//6.9e-50:381.83/Hs.161917:AA483223
R-THYRO1000605/ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483.96/Hs.21907:N24415
R-THYRO1000625/ESTs/5.6e-36:257.84/Hs.139657:AA191742
R-THYRO1000637
R-THYRO1000641/ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens]//4.9e-46:245.95/Hs.97398:AA398634
R-THYRO1000658/ESTs//5.8e-48:281.90/Hs.142259:AA828840
R-nnnnnnnnnnnn/ESTs/1.5e-82:389.99/Hs.155573:AA487384
R-THYRO1000666/ESTs//1.4e-26:179.88/Hs.98382:AA479866
R-THYRO1000676/EST//6.4e-05:88.77/Hs.133242:AO61063
R-THYRO1000684/ESTs/1.9e-69:374.94/Hs.144617:R77109
R-THYRO1000699/ESTs//1.7e-58:394.86/Hs.26373:AA700713
R-THYRO1000712
R-THYRO1000734/EST//2.0e-06:95.73/Hs.156201:AA724287
R-THYRO1000748/EST//4.1e-12:155.74/Hs.118694:AA148713
R-THYRO1000756/ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2-3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497.87/Hs.109672:W22624
R-THYRO1000777
R-THYRO1000783/EST//5.6e-100:470.99/Hs.123515:AA812932
R-THYRO1000787/EST//8.0e-34:175.99/Hs.99607:AA463897
R-THYRO1000793/ESTs/2.2e-106:505.99/Hs.50929:AA4443144
R-THYRO1000796/ESTs/4.3e-44:445.75/Hs.55855:AA621381
R-THYRO1000805/EST//2.6e-32:407.67/Hs.123244:AA183594
R-THYRO1000815/Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307.87/Hs.22271:D26067

- R-THYRO1000829
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
 5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
 10 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
 15 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881
 R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI020777
 20 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
 R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
 25 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
 R-THYRO1001100
 R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-66:491:89//Hs.89135:AI138834
 30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
 R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
 35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
 R-THYRO1001177
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
 R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA079151
 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA826932
 40 R-THYRO1001262//Human kpnl repeatmna (cdna clone pcd-kpnl-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
 45 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642
 R-THYRO1001362
 R-THYRO1001363//ESTs//0.16:422:5.9//Hs.23876:AA082935
 R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
 50 R-THYRO1001365
 R-THYRO1001374
 R-THYRO0014011//Human HsLIM15 mRNA for HsLIM15, complete cds//2.5e-48:467:75//Hs.37181:D64108
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
 55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977

- R-THYRO1001434//ESTs//0.40:161.61//Hs.161993:AA503172
 R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082
- 5 R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331.79//Hs.155464:AF088219
 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110
 R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094
- 10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936
 R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594
 R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413
 R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958
- 15 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741
 R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedin C)//7.4e-12:288:67//Hs.85112:X57025
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:di-hydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190
- 20 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874
 R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282
 R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform/-1.6e-111:562:95//Hs.118633:AJ225089
- 25 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
 R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726
 R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691
- 30 R-THYRO1001721
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172
 R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323
 R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474
- 35 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224
 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956
 R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123
- 40 R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
 R-VESEN1000122
 R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289
 R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321
- 45 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540
 R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629
 R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792
- 50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991
 R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103
 R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812
- 55 R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624
 R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363
 R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

R-Y79AA1000328//ESTs/1.9e-76:448.91/Hs.16470:AA6412635
R-Y79AA1000342//ESTs, Weakly similar to MATRN3 [H.sapiens]/J.0e-37:239.88/Hs.23476:AA401210
R-Y79AA1000346//ESTs/J.9e-12:139.76/Hs.151987:AA483808
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]/
4.4e-66:339.97/Hs.8215:AA521150
R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/J.3.2e-
44:279.88/Hs.139007:H74314
R-Y79AA1000368//ESTs/J.8e-97:513.94/Hs.68090:AA641018
R-Y79AA1000405//ESTs/J.4e-47:267.94/Hs.125304:R51613
R-Y79AA1000410//ESTs/J.4e-49:359.82/Hs.158107:AA707758
R-Y79AA1000420//EST/J.0.17:69.69/Hs.160859:A1352292
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]/J.3.1e-
60:362.88/Hs.6381:A1188509
R-Y79AA1000480//ESTs/J.1.0e-75:433.91/Hs.78110:AA741320
R-Y79AA1000538//EST/J.7e-48:307.87/Hs.149580:A1281881
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds/J.95:172:62/Hs.
41723:U37426
R-Y79AA1000540//ESTs/J.1.5e-97:534.93/Hs.67991:AA147848
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]/J.8.2e-97:482.97/Hs.19121:
A1125280
R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]/J.1.3e-107:564.93/Hs.16361:A1147455
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds/J.3.4e-99:517.94/Hs.60580:
AF060503
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN AT51-TPD3 INTERGENIC
REGION [Saccharomyces cerevisiae]/J.8.1e-27:140.100/Hs.129049:H28818
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds/J.8.7e-114:586:
95/Hs.83023:AF093670
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III
[C.elegans]/J.9.8e-111:563.95/Hs.19845:A1005330
R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds/J.0.97:235.59/Hs.1701:L26405
R-Y79AA1000774//ESTs/J.5.9e-109:559.95/Hs.17138:N91463
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds/J.1.6e-18:107.100/Hs.84753:D87433
R-Y79AA1000784//EST/J.0.80:87:67/Hs.158558:A1368359
R-Y79AA1000794//ESTs/J.2.7e-99:498.96/Hs.25441:AA580512
R-Y79AA1000800//ESTs/J.1.2e-97:532.93/Hs.17822:AA532642
R-nnnnnnnnnnnn/Carboxypeptidase E/J.0.18:354:59/Hs.75360:X51405
R-Y79AA1000805
R-Y79AA1000824//ESTs/J.0.99:276.61/Hs.153992:AA280227
R-Y79AA1000827//ESTs/J.1.2e-55:326.92/Hs.158127:A1334650
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds/J.0.016:386:59/Hs.
55836:U85647
R-Y79AA1000962//EST/J.0.024:177.63/Hs.25214:R37079
R-Y79AA1000968
R-Y79AA1000969//ESTs/J.2.9e-70:251.98/Hs.120858:AA417181
R-Y79AA1000976//ESTs/J.7.8e-56:299.95/Hs.120125:M86049
R-Y79AA1000985
R-Y79AA1001023//ESTs/J.5.7e-66:379.90/Hs.64616:W22851
R-Y79AA1001041//ESTs/R.6e-06:54:100/Hs.8980:AA629067
R-Y79AA1001048//ESTs/J.4.4e-97:461.99/Hs.7010:AA837407
R-Y79AA1001061//ESTs/J.3.8e-105:493.99/Hs.128419:A271325
R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds/J.4.8e-53:279.83/Hs.15731:
AB011135
R-Y79AA1001077//ESTs/J.1.9e-51:339.87/Hs.11197:AA309047
R-Y79AA1001078//ESTs/R.3e-98:528.92/Hs.24608:AA161260
R-Y79AA1001105//ESTs/J.6.0e-77:393.96/Hs.30837:H08155
R-Y79AA1001145//ESTs/J.1.7e-13:285.64/Hs.128259:AA343015
R-Y79AA1001167
R-Y79AA1001177//EST/J.1.2e-05:92.76/Hs.65277:T15884

R-Y79AA1001186
R-Y79AA1001211//ESTs//1.3e-70;344.97//Hs.49760;AA74A051
R-Y79AA1001216//ESTs//5.8e-63;416.88//Hs.8595;W60933
R-Y79AA1001228//ESTs//9.3e-101;483.98//Hs.13916;AI025750
R-Y79AA1001233//EST//0.00027;232.62//Hs.132431;AA909674
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNC101133Q7) (RZPD Berlin)//1.e-110;549.95//Hs.23170;AJ005892
R-Y79AA1001281//ESTs//3.6e-98;466.99//Hs.104442;AA481271
R-Y79AA1001299//Human Inr1 mRNA, complete cds//9.6e-25;133.100//Hs.155626;U04847
R-Y79AA1001312//ESTs//3.4e-92;454.97//Hs.127319;AI191149
R-Y79AA1001323//ESTs//1.6e-67;422.89//Hs.118559;AA87084
R-Y79AA1001384//ESTs//3.1e-104;496.98//Hs.153695;AA004143
R-Y79AA1001391//ESTs//2.2e-77;418.94//Hs.118608;AA101819
R-Y79AA1001394//ESTs//2.1e-78;409.95//Hs.23413;AA579859
R-Y79AA1001402//EST//9.3e-08;128.75//Hs.141607;N63891
R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109;553.95//Hs.106616;AI027524
R-Y79AA1001511//ESTs//4.9e-49;271.92//Hs.109045;AA523704
R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46;260.94//Hs.24884;AA176812
R-nnnnnnnnnnnn//EST//0.62;126.67//Hs.137020;AA868563
R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95;517.91//Hs.76987;AF012872
R-Y79AA1001555//Collagen, type XI, alpha 1//1.0e-157;64/Hs.82772;J04177
R-Y79AA1001585//ESTs//1.9e-90;430.98//Hs.48333;AA704508
R-Y79AA1001594//ESTs//9.6e-23;122.100//Hs.63795;AI126237
R-Y79AA1001603//ESTs//1.0e-50;193.100//Hs.25635;AI336204
R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81;400.97//Hs.13323;AA897542
R-Y79AA1001647//ESTs, 6.9e-92;479.95//Hs.154270;N26486
R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19;112.97//Hs.26252;AA643235
R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99;553.92//Hs.108896;R54040
R-nnnnnnnnnnnn
R-Y79AA1001696//ESTs//1.4e-84;478.91//Hs.6606;AA211783
R-Y79AA1001705//ESTs//6.7e-107;546.95//Hs.106805;AA418490
R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085;251.63//Hs.21864;AL031652
R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87;427.97//Hs.18645;AI023798
R-nnnnnnnnnnnn//ESTs//1.1e-112;558.97//Hs.109755;AA180809
R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae Y9D335.03c protein [H.sapiens]//8.1e-95;530.91//Hs.72444;W23217
R-Y79AA1001846//EST//2.8e-41;312.81//Hs.162236;AA551582
R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54;221.58//Hs.99931;L34355
R-Y79AA1001866//ESTs//2.2e-102;498.97//Hs.130683;AI278630
R-Y79AA1001874//ESTs//1.9e-76;377.98//Hs.79707;AA354094
R-Y79AA1001875//ESTs//0.64;152.63//Hs.156159;AI333652
R-Y79AA1001923//EST//0.19;180.58//Hs.148290;AA908404
R-Y79AA1002027//ESTs//1.6e-104;497.98//Hs.21275;T73275
R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69;93.73//Hs.15731;AB011135
R-Y79AA1002089//Homo sapiens PYRJIN (MEFV) mRNA, complete cds//1.1e-46;392.80//Hs.113283;AF018080
R-Y79AA1002093//Homo sapiens CT198 mRNA, complete ORF//1.2e-12;80.100//Hs.78185;L38933
R-Y79AA1002103//ESTs//1.3e-52;535.76//Hs.142167;AI417785
R-Y79AA1002115//ESTs//4.2e-101;519.96//Hs.23977;AA115275
R-Y79AA1002125//ESTs//9.8e-68;363.94//Hs.72085;AA193399
R-Y79AA1002139//ESTs//1.2e-80;498.96//Hs.72020;AA149858
R-Y79AA1002204//ESTs//2.1e-83;434.95//Hs.22979;R43725

30 Homology Search Result Data 6

35 mology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark //

C-HEMBA1000387
C-HEMBA1000392

C-HEMBA1000460
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279
 5 C-HEMBA1000501
 C-HEMBA1000508
 C-HEMBA1000520
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-
 MENTS).//2.6E-12//73aa//41%//P02826
 10 C-HEMBA1000534
 C-HEMBA1000555
 C-HEMBA1000568
 C-HEMBA1000588
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295
 15 C-HEMBA1000636
 C-HEMBA1000682
 C-HEMBA1000686
 C-HEMBA1000719
 C-HEMBA1000727
 C-HEMBA1000752
 20 C-HEMBA1000817
 C-HEMBA1000851
 C-HEMBA1000867
 C-HEMBA1000869
 C-HEMBA1000872
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//
 1.6E-30//127aa//40%//P43366
 C-HEMBA1000918
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-
 MOSOME X.//1E-10//288aa//23%//Q19124
 30 C-HEMBA1000946
 C-HEMBA1000968
 C-HEMBA1000971
 C-HEMBA1000975
 C-HEMBA1001009
 35 C-HEMBA1001022
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//
 1.4E-12//131aa//38%//Q01485
 C-HEMBA1001052
 C-HEMBA1001080
 40 C-HEMBA1001085
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//
 176aa//57%//P48059
 C-HEMBA1001109
 C-HEMBA1001122
 45 C-HEMBA1001133
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
 (FRAGMENT).//1.5E-116//197aa//58%//Q06730
 C-HEMBA1001140
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//
 AB020678
 C-HEMBA1001235
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
 C-HEMBA1001281
 55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//
 29%//Q60401
 C-HEMBA1001303
 C-HEMBA1001310

C-HEMBA1001326
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358
 5 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
 C-HEMBA1001388
 C-HEMBA1001398
 C-HEMBA1001405
 C-HEMBA1001407
 10 C-HEMBA1001413
 C-HEMBA1001415
 C-HEMBA1001446
 C-HEMBA1001450
 C-HEMBA1001455
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850
 15 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
 C-HEMBA1001533
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
 C-HEMBA1001581
 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450
 25 C-HEMBA1001702
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386
 C-HEMBA1001731
 C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009
 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
 C-HEMBA1001815
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
 C-HEMBA1001864
 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342
 C-HEMBA1001987
 C-HEMBA1002018
 40 C-HEMBA1002049
 C-HEMBA1002084
 C-HEMBA1002125
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293
 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694
 C-HEMBA1002191
 C-HEMBA1002199
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161
 50 C-HEMBA1002237
 C-HEMBA1002265
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
 C-HEMBA1002349
 55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
 C-HEMBA1002430

- C-HEMBA1002439
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%/Q00994
 C-HEMBA1002460
 C-HEMBA1002462
- 5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%/P98175
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%/P17437
 C-HEMBA1002477
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%/P48732
- 10 C-HEMBA1002515
 C-HEMBA1002542
 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%/AF075587
 C-HEMBA1002583
- 15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%/AB011169
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%/AB018351
 C-HEMBA1002688
 C-HEMBA1002696
 C-HEMBA1002750
- 20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%/AJ000414
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%/AB020636
 C-HEMBA1002777
 C-HEMBA1002794
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2E-314//1437bp//99%/AF071185
- 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%/AJ132819
 C-HEMBA1002850
 C-HEMBA1002863
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%/Q09297
- 30 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%/AB011148
 C-HEMBA1002937
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%/P16157
- 35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%/AB020710
 C-HEMBA1002954
 C-HEMBA1002971
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%/P14646
- 40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%/Q02224
 C-HEMBA1003033
 C-HEMBA1003035
 C-HEMBA1003041
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%/O75439
- 45 C-HEMBA1003067
 C-HEMBA1003096
 C-HEMBA1003117
 C-HEMBA1003129
- 50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%/P41940
 C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%/AL079278
- 55 C-HEMBA1003175
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%/P44551
 C-HEMBA1003199

- C-HEMBA1003222
 C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%/Q02088
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%/Q06548
- 5 C-HEMBA1003257
 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%/P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%/AB024436
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%/AB011109
- 10 C-HEMBA1003322
 C-HEMBA1003327
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0000002//248aa//23%/Q02224
 C-HEMBA1003370
 C-HEMBA1003380
 C-HEMBA1003395
- 15 C-HEMBA1003402
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%/AB020712
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6E-312//1414bp//99%/AL050287
 C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%/P37709
- 20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139
 C-HEMBA1003447
 C-HEMBA1003461
 C-HEMBA1003463
 C-HEMBA1003528
- 25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%/P50480
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%/P53384
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I);G(S);G(O) GAMMA-2 SUBUNIT (G GAMMA-1).//1.2E-31//71aa//100%/P16874
 C-HEMBA1003568//52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%/P19474
- 30 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%/Q13330
 C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%/P26039
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//35%/P19682
- 35 C-HEMBA1003615
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%/AB015344
 C-HEMBA1003621
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%/Q13207
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%/P53973
- 40 C-HEMBA1003711
 C-HEMBA1003807
 C-HEMBA1003864
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%/P16372
- 45 C-HEMBA1003959
 C-HEMBA1003989
 C-HEMBA1004074
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%/AF091234
- 50 C-HEMBA1004146
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%/AB023145
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/U50748
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%/AF095927
- 55 C-HEMBA1004246
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//99%/AF092094
 C-HEMBA1004289

EP 1 074 617 A2

C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841
 5 C-HEMBA1004596
 C-HEMBA1004693
 C-HEMBA1004736
 C-HEMBA1004753
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//1515bp//86%//U49082
 10 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//L39060
 C-HEMBA1004763
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547
 C-HEMBA1004771
 C-HEMBA1004776
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P05851
 C-HEMBA1004806
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//Q00004
 C-HEMBA1004850
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//100%//AL080114
 C-HEMBA1004923
 C-HEMBA1004929
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401
 25 C-HEMBA1004933
 C-HEMBA1004954
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036
 C-HEMBA1005475
 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%//P16372
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043
 C-HEMBA1006377
 C-HEMBA1006467
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552
 C-HEMBA1006530
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.00000043//111aa//40%//Q01485
 C-HEMBA1006795
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258
 C-HEMBA1006936
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//AP078849
 C-HEMBA1007342
 C-HEMBA1000008
 C-HEMBA1000018
 50 C-HEMBA1000024
 C-HEMBA1000025
 C-HEMBA1000036
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928
 55 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799
 C-HEMBA1000103
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEM BB1000136
 C-HEM BB1000215
 C-HEM BB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEED8.5.//
 2.7E-12//112aa//47%//Q09530
 5 C-HEM BB1000244
 C-HEM BB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-
 MOSOME V.//6.1E-09//242aa//26%//Q23256
 C-HEM BB1000338
 C-HEM BB1000339
 10 C-HEM BB1000391
 C-HEM BB1000438
 C-HEM BB1000449
 C-HEM BB1000589
 C-HEM BB1000591
 15 C-HEM BB1000623
 C-HEM BB1000630
 C-HEM BB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//
 232aa//28%//P78970
 C-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
 20 C-HEM BB1000671
 C-HEM BB1000673
 C-HEM BB1000705
 C-HEM BB1000706
 C-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//
 U53475
 25 C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
 C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//
 1.2E-126//613bp//97%//AF111105
 C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-
 54//232aa//43%//P39956
 30 C-HEM BB1000807
 C-HEM BB1000810
 C-HEM BB1000848
 C-HEM BB1000852
 35 C-HEM BB1000870
 C-HEM BB1000887
 C-HEM BB1000908
 C-HEM BB1000927//Homo sapiens calseinlin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
 C-HEM BB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//
 99%//AF116910
 40 C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
 C-HEM BB1000975
 C-HEM BB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-
 18//178aa//30%//P28575
 45 C-HEM BB1000991
 C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//
 P51523
 C-HEM BB1001014
 C-HEM BB1001024
 50 C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED
 NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
 C-HEM BB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//
 80%//AF010144
 C-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
 55 C-HEM BB1001096
 C-HEM BB1001105
 C-HEM BB1001117
 C-HEM BB1001126

- C-HEM BB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//01/3069bp/99%//AB019435
 C-HEM BB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp/76%//AF110267
- 5 C-HEM BB1001153
 C-HEM BB1001169
 C-HEM BB1001175//ANKYRIN.//6.9E-11//169aa/31%//Q02357
 C-HEM BB1001182
 C-HEM BB1001199
- 10 C-HEM BB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//01/1816bp/99%//AB023187
 C-HEM BB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897
 C-HEM BB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp/99%//AF132966
 C-HEM BB1001289
- 15 C-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081
 C-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703
 C-HEM BB1001331
 C-HEM BB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175
- 20 C-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp/99%//AF097441
 C-HEM BB1001369
 C-HEM BB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//01/1586bp/99%//AF100757
 C-HEM BB1001387
 C-MAMMA1002317
- 25 C-MAMMA1002319
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.0000015//206aa//29%//Q02926
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190
 C-NT2RM1000042
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028
- 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942
 C-NT2RM1000669
 C-NT2RM1000781
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp/99%//AF092138
- 35 C-NT2RM1001008
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.00000002//980bp/95%//AF085360
 C-NT2RM1001074
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//
- 40 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence.//01/1740bp/99%//AL031291
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.0000043//136aa//31%//P54703
- 45 C-NT2RM2000032
 C-NT2RM2000042
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102
- 50 C-NT2RM2000093
 C-NT2RM2000101
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//01/1574bp/99%//AF067223
 C-NT2RM2000192
 C-NT2RM2000239
- 55 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2E-314//1416bp//100%//AL080069
 C-NT2RM2000259

- C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//3.6E-19//181-aa//34%//P14918
- C-NT2RM2000287
- 5 C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//AB020666
- C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132
- C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN //1.8E-14//245aa//29%//P11274
- C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251
- 10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE)//1.7E-68//419aa//36%//P50849
- C-NT2RM2000374
- C-NT2RM2000395
- 15 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT)//1.6E-54//344aa//33%//P32802
- C-NT2RM2000407
- C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//Q08469
- 20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION//0.0000001//157aa//28%//P36113
- C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-)//0.0000089//377aa//24%//P22211
- C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823
- 25 C-NT2RM2000502
- C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243
- C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%//P17437
- C-NT2RM2000540
- 30 C-NT2RM2000567
- C-NT2RM2000569
- C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.7E-187//741aa//46%//P73505
- C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987
- 35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973
- C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487
- C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//AF179221
- 40 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%//Q08170
- C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272
- C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558
- C-NT2RM2000639
- 45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576
- C-NT2RM2000669
- C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391
- C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//36%//Q15404
- 50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342
- C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//P41877
- C-NT2RM2000795
- C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//98%//P23514
- 55 C-NT2RM2000837
- C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//AB015046

- C-NT2RM2000952
C-NT2RM2000984
C-NT2RM2001004
C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809
5 C-NT2RM2001065
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//26%//P46577
C-NT2RM2001131
C-NT2RM2001141
10 C-NT2RM2001152
C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//1335bp//99%//AL080109
C-NT2RM2001194
C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143
15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//P48724
C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//32%//P97924
C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%//P13264
20 C-NT2RM2001243
C-NT2RM2001247
C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//P53995
25 C-NT2RM2001291
C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//AL080063
C-NT2RM2001312
C-NT2RM2001319
30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584
C-NT2RM2001345//VEGETATILE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808
C-NT2RM2001370
C-NT2RM2001393
C-NT2RM2001420
35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//100%//AL050146
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//437aa//57%//P52569
C-NT2RM2001504
40 C-NT2RM2001524
C-NT2RM2001544
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//90aa//42%//P38660
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-61//312aa//44%//P19474
45 C-NT2RM2001582
C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692
C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931
50 C-NT2RM2001930
C-NT2RM2001935
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250
55 C-NT2RM2001982
C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//P37838
C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

- 28%//Q12730
C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%//Q09782
- 5 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.00000029//83aa//44%//P40796
C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%//P46837
C-NT2RM2002030//Homo sapiens mRNA for Glutamine-fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789
- 10 C-NT2RM2002049
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%//Q61990
- 15 C-NT2RM2002091
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%//P49695
- 20 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN C12.//8E-31//105aa//47%//P47805
C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%//AL117402
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167
- 25 C-NT2RM4000061
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742
C-NT2RM4000139//R. norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%//P25386
- 30 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%//P16381
C-NT2RM4000197
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255
C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%//L20303
- 35 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%//M99438
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637
- 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246
C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412
C-NT2RM4000395
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
- 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//24%//Q10297
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280
- 50 C-NT2RM4000498//SAP1 PROTEIN.//8.3E-53//434aa//29%//P39955
C-NT2RM4000511
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%//P16884
- 55 C-NT2RM4000520
C-NT2RM4000585
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%//AF186273
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

- C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657
 C-NT2RP1000040
 C-NT2RP1000063
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834
 5 C-NT2RP1000101
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471
 C-NT2RP1000112
 C-NT2RP1000124
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165
 C-NT2RP1000170
 C-NT2RP1000191
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357
 C-NT2RP1000243
 15 C-NT2RP1000259
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343
 C-NT2RP1000357
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159
 C-NT2RP1000416
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257
 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653
 C-NT2RP1000481
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020
 C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367
 40 C-NT2RP1000581
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233
 C-NT2RP1000688
 C-NT2RP1000695
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960
 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223
 C-NT2RP1000846
 C-NT2RP1000851
 55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-

- 105//504bp//99%//UJ39317
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//M17885
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338
 C-NT2RP1000980
 C-NT2RP1000988
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//1529bp//61%//L01790
 C-NT2RP1001014
 C-NT2RP1001395
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917
 C-NT2RP1001424
 C-NT2RP1001449
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%//AJ005257
 C-NT2RP1001466
 C-NT2RP1001475
 C-NT2RP1001482
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//I035566
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%//P47758
 C-NT2RP1001616
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594
 C-NT2RP2000008//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%//O34136
 C-NT2RP2000007
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//P51523
 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//34%//Q01730
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749
 C-NT2RP2000054
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP-EP-SILON).//9.4E-16//45aa//100%//P49446
 C-NT2RP2000067
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//383aa//32%//P33450
 C-NT2RP2000079
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338
 C-NT2RP2000091
 C-NT2RP2000097
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
 C-NT2RP2000120
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//P41877
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-147 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891
 C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

EP 1 074 617 A2

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//
 AB023225
 C-NT2RP2000173
 C-NT2RP2000175
 C-NT2RP2000195
 C-NT2RP2000205
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568
 C-NT2RP2000232
 C-NT2RP2000233
 C-NT2RP2000239
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558
 C-NT2RP2000270
 C-NT2RP2000274
 C-NT2RP2000283
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//
 25%//Q10297
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676
 C-NT2RP2000298
 C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//
 1193bp//99%//U82381
 C-NT2RP2000328
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
 226aa//92%//P08760
 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//
 674aa//46%//P17564
 C-NT2RP2000369
 C-NT2RP2000412
 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//
 100%//P52597
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//11757bp//
 99%//AF102265
 C-NT2RP2000438
 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844
 C-NT2RP2000503
 C-NT2RP2000510
 C-NT2RP2000516
 C-NT2RP2000603
 C-NT2RP2000617
 C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514
 C-NT2RP2000656
 C-NT2RP2000658
 C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
 C-NT2RP2000704
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.7E-100//
 488aa//44%//O32038
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680
 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//
 29%//Q99104
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//
 P13466
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174
 C-NT2RP2000819
 C-NT2RP2000841
 C-NT2RP2000845
 C-NT2RP2000863

C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/060841
 C-NT2RP2000892
 C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%/AL050390
 C-NT2RP2000938
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%/AB018298
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
 C-NT2RP2000985
 C-NT2RP2001036
 C-NT2RP2001044
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%/AB007957
 C-NT2RP2001065
 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.8E-46//222aa//45%/P14105
 C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232
 C-NT2RP2001094
 C-NT2RP2001119
 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
 C-NT2RP2001218
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.2E-10//366aa//28%/P14105
 C-NT2RP2001381
 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp//100%/AL080146
 C-NT2RP2001427
 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%/AB018340
 C-NT2RP2001675
 C-NT2RP2001721
 C-NT2RP2001907
 C-NT2RP2001969
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378
 C-NT2RP2002046
 C-NT2RP2002154
 C-NT2RP2002208
 C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%/P42568
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521
 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%/AB015594
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958
 C-NT2RP2002426
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289
 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815
 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345
 C-NT2RP2002621
 C-NT2RP2002672
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%/O14345
 C-NT2RP2002769
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764

- C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392
- C-NT2RP2002954
- 5 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669
- C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129
- C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190
- 10 C-NT2RP2003108
- C-NT2RP2003117
- C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//AF079765
- C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652
- C-NT2RP2003177
- 15 C-NT2RP2003194
- C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
- C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572
- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337
- 20 C-NT2RP2003367
- C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378
- C-NT2RP2003446
- C-NT2RP2003533
- 25 C-NT2RP2003543//HYPOTHETICAL tRNA/tRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261
- C-NT2RP2003596
- C-NT2RP2003629
- C-NT2RP2003687
- 30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481
- C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669
- C-NT2RP2003793
- 35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175
- C-NT2RP2003986
- C-NT2RP2004042
- 40 C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820
- C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120
- C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044
- C-NT2RP2004463
- 45 C-NT2RP2004602
- C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139
- C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291
- C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.6E-64//616aa//33%//Q92355
- 50 C-NT2RP2004791//PUTATIVE LEUCYL-tRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- tRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490
- C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588
- C-NT2RP2004802
- 55 C-NT2RP2004841
- C-NT2RP2004936
- C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692
- C-NT2RP2004999

- C-NT2RP2005000
 C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515
 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447
 5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743
 C-NT2RP2005140
 C-NT2RP2005147
 C-NT2RP2005159
 10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025
 C-NT2RP2005270
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053
 C-NT2RP2005293
 C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576
 15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
 C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170
 20 C-NT2RP2005441
 C-NT2RP2005453
 C-NT2RP2005464
 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127
 C-NT2RP2005472
 25 C-NT2RP2005495
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563
 30 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526
 C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963
 C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366
 35 C-NT2RP2005555
 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529
 C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%//AF062085
 40 C-NT2RP2005622
 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623
 C-NT2RP2005637
 C-NT2RP2005640
 45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//IP5601
 C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973
 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814
 C-NT2RP2005683
 50 C-NT2RP2005690
 C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342
 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.00000003//169aa//28%//IP38074
 C-NT2RP2005748
 55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868
 C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

- C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943
 C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%//AF151351
- 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038
 C-NT2RP2005781
 C-NT2RP2005804
- 10 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223
 C-NT2RP2005853
 C-NT2RP2005868
 C-NT2RP2005886
 C-NT2RP2005890
- 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837
 C-NT2RP2006038
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%//Q08170
- 20 C-NT2RP2006052
 C-NT2RP2006069
 C-NT2RP2006071
 C-NT2RP2006100//Homo sapiens mRNA: cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1758bp//99%//AL049970
- 25 C-NT2RP2006106
 C-NT2RP2006141
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.E-189//899bp//97%//AB014554
 C-NT2RP2006196
 C-NT2RP2006200
- 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484
 C-NT2RP2006237
 C-NT2RP2006238
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%//P46821
- 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262
 C-NT2RP2006333
 C-NT2RP2006365
 C-NT2RP2006393
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//0.00000034//50aa//50%//Q61658
- 40 C-NT2RP2006456
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
 C-NT2RP2006467
 C-NT2RP2006472
- 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP1G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//168aa//25%//P09543
- 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708
 C-NT2RP3000072
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164
 C-NT2RP3000220
 C-NT2RP3000251
- 55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
 C-NT2RP3000312
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

- C-NT2RP3000333
C-NT2RP3000348
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN
HP0303./0.00000028//185aa//31%//O25074
- 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2E-111//226aa//92%//P08760
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6./0//2072bp//98%//AB019219
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18./2.1E-107//206aa//99%//P35293
- 10 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.7E-139//679aa//41%//O43143
C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds./0//2364bp//99%//AF071185
C-NT2RP3000484
C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)./4.8E-28//536aa//27%//P28160
- 15 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN)./1.9E-12//192aa//30%//P15151
C-NT2RP3000596//TRICHOHYALIN./2.5E-17//304aa//28%//Q07283
C-NT2RP3000599
C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)./3E-140//499aa//46%//P51523
- 20 C-NT2RP3000644
C-NT2RP3000661
C-NT2RP3000665
C-NT2RP3000690
C-NT2RP3000759//ADP-RIBOSYLATION FACTOR./7E-28//176aa//34%//Q94650
- 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN./2.5E-36//417aa//31%//Q61982
C-NT2RP3000836
C-NT2RP3000841
C-NT2RP3000850
C-NT2RP3000852
C-NT2RP3000859
- 30 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds./6.9E-69//1611bp//61%//U53445
C-NT2RP3000869
C-NT2RP3000901
C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds./0//3199bp//99%//AF064257
- 35 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds./2.7E-185//585bp//88%//AF015264
C-NT2RP3000980
C-NT2RP3000994//MATERNAL EFFECT PROTEIN
STAUFEN./0.00000006//78aa//48%//P25159
- 40 C-NT2RP3001004
C-NT2RP3001081
C-NT2RP3001084
C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds./1.7E-94//787bp//66%//AF087433
- 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN)./3E-44//260aa//40%//P55201
C-NT2RP3001109
C-NT2RP3001116
C-NT2RP3001119
C-NT2RP3001133
- 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds./0//2802bp//99%//AB018305
C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein./0//2732bp//99%//AJ006266
C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION./1.7E-10//196aa//27%//P53154
C-NT2RP3001214
- 55 C-NT2RP3001216//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)./0.0000023//137aa//33%//P35663
C-NT2RP3001221//GAMMA-BUTYROBETAINE-2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE)./1.9E-31//353aa//30%//P80193

- C-NT2RP3001236
C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1]//1.2E-166//395aa//51%/P14873
- 5 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%/AB020718
C-NT2RP3001307
C-NT2RP3001325
C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%/AB025905
C-NT2RP3001392
- 10 C-NT2RP3001396
C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF//1.3E-61//374aa//36%/P49711
C-NT2RP3001407//SCY1 PROTEIN//0.00000033//143aa//25%/P53009
C-NT2RP3001420
C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT)//1E-16//77aa//46%/O33529
- 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG//2.7E-10//159aa//33%/O09053
C-NT2RP3001457
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//9.1E-13//87aa//43%/P11632
C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%/U13395
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%/AF064801
- 20 C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN//1E-61//345aa//42%/P20964
C-NT2RP3001621
C-NT2RP3001629
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210//6.8E-18//91aa//38%/Q92609
- 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2//8.8E-09//132aa//31%/O22468
C-NT2RP3001676
C-NT2RP3001679
C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE//1.6E-11//348aa//279%/P24733
C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)//1.7E-18//249aa//30%/Q04652
- 30 C-NT2RP3001896
C-NT2RP3001915
C-NT2RP3001929
C-NT2RP3003193//ZINC FINGER PROTEIN 135//7.3E-98//269aa//62%/P52742
C-NT2RP3004466
- 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.3E-113//466aa//42%/P34110
C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%/AB014532
C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%/AB011126
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)//0.00000038//150aa//28%/Q01484
- 40 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%/AF026445
C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%/AB007946
C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%/AJ006266
C-NT2RP3004617//ZINC-BINDING PROTEIN A33//7.2E-75//464aa//35%/Q02084
- 45 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%/AF093097
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)//1.7E-72//254aa//45%/P54352
- 50 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64//2.6E-98//239aa//64%/P35526
C-NT2RP40000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65//4.9E-51//335aa//37%/Q64375
C-NT2RP40000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%/AB020657
C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%/AB011538
C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//0//728aa//99%/Q10568
- 55 C-NT2RP4000129
C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%/AF011427

C-NT2RP4000150
 C-NT2RP4000151
 C-NT2RP4000159
 C-NT2RP4000185
 5 C-NT2RP4000212//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//P15287
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173
 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.5E-26//237aa//28%//Q01631
 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372
 C-NT2RP4000355
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
 20 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243
 C-NT2RP4000381
 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738
 C-NT2RP4000415
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078
 30 C-NT2RP4000449
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%//P50101
 35 C-NT2RP4000480
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484
 40 C-NT2RP4000500
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818
 C-NT2RP4000524
 C-NT2RP4000541
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319
 45 C-NT2RP4000560
 C-NT2RP4000588
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730
 C-NT2RP4000638
 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625
 C-NT2RP4000704
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//Q11073
 55 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148
 C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0/3574bp//99%//AB023229
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//
 0.00000032//67aa//31%//P53915
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0/1927bp//99%//AB007939
 5 C-NT2RP4000833
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265
 C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175
 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//
 227aa//36%//Q06828
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-
 ZYME 1).//1.5E-76//346aa//43%//Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900
 20 C-NT2RP4000955
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//
 90aa//42%//P38660
 C-NT2RP4000975
 C-NT2RP4000979
 25 C-NT2RP4000984
 C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968
 30 C-NT2RP4001006
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.5E-
 92//443aa//44%//Q09996
 C-NT2RP4001057
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//
 563aa//46%//P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967
 C-NT2RP4001086
 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400
 C-NT2RP4001100
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//
 P36378
 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP).//0.00000021//
 93aa//33%//P44514
 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//
 3.4E-29//385aa//29%//P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
 4.7E-29//227aa//35%//P52178
 55 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//
 65%//U95760
 C-NT2RP4001207

- C-NT2RP4001210
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%//P38660
 5 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652
 C-NT2RP4001235
 C-NT2RP4001256
 C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682
 C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082
 10 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%//Q07283
 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391
 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%//AJ001119
 15 C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014
 C-NT2RP4001343
 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%//AB017494
 C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445
 20 C-NT2RP4001353
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-19//222aa//30%//Q08180
 C-NT2RP4001373
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//9.2E-17//146aa//35%//P18160
 25 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1.//12E-53//436aa//30%//Q10085
 C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141
 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q99676
 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//AF129131
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010
 C-NT2RP4001502
 C-NT2RP4001507
 C-NT2RP4001524
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3.8%//P25656
 40 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF152961
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.0000054//213aa//26%//Q02453
 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197
 C-NT2RP4001571
 C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%//P73505
 50 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676
 C-NT2RP4001614
 C-NT2RP4001634
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469
 55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323
 C-NT2RP4001677
 C-NT2RP4001679
 C-NT2RP4001696//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

- 100 KD SUBUNIT).//4E-10//243aa//25%//Q10568
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//Q10282
 5 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-10//1168aa//33%//Q09332
 C-NT2RP4001739
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//865aa//58%//P51523
 10 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232
 C-NT2RP4001803
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566
 15 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083
 C-NT2RP4001828
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555bp//73%//AF155595
 C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709
 20 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFpZp5640043 (from clone DKFpZp5640043).//0//1306bp//98%//AL050390
 C-NT2RP4001896//VEGETABLE INCOMPATIBILITY PROTEIN HET-E1.//0.00000014//345aa//25%//Q00808
 C-NT2RP4001901
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024
 25 C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816
 30 C-NT2RP4001953
 C-NT2RP4001966
 C-NT2RP4001975
 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652
 C-NT2RP4002052
 35 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1E-137//679aa//40%//Q43143
 C-NT2RP4002071
 C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//1722aa//39%//Q05481
 40 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655
 C-NT2RP4002298
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938
 C-NT2RP4002791
 45 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFpZp434F172 (from clone DKFpZp434F172).//0//2557bp//99%//AL080202
 C-NT2RP4002905
 C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552
 C-NT2RP5003477//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808
 50 C-NT2RP5003492
 C-NT2RP5003500
 C-NT2RP5003506
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//P37116
 55 C-NT2RP5003524
 C-NT2RP5003534
 C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

O14727
 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922
 C-OVARC1000035
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//
 5 0.0000032//60aa//45 %//P80022
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//
 8.4E-14//259aa//30%//P51610
 C-OVARC1000113
 10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955
 C-OVARC1000148
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//
 2.5E-95//461bp//98%//AJ242975
 C-OVARC1000168
 15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//
 AF068332
 C-OVARC1000212
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665
 20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-
 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//
 30%//P14904
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363
 25 C-OVARC1000321
 C-OVARC1000326
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//
 200aa//27%//P40004
 C-OVARC1000347
 30 C-OVARC1000384
 C-OVARC1000411
 C-OVARC1000420
 C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205
 C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//
 35 99%//AL080126
 C-OVARC1000461
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075
 C-OVARC1000466
 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452
 C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850
 C-OVARC1000564
 C-OVARC1000576
 45 C-OVARC1000588
 C-OVARC1000605
 C-OVARC1000640
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-
 plete cds.//0//1812bp//98%//D43772
 50 C-OVARC1000661
 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886
 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978
 55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946
 C-OVARC1001162
 C-OVARC1001243
 C-OVARC1001296